

R;Accession: UC013
 R;Takahashi, T.; Sugihita, Y.; Nojiri, T.; Shimizu, T.; Yao, A.; Kinugawa, K.; Harada, Biochem. Biophys. Res. Commun. 281: 1057-1062, 2001
 A;Title: Cloning of hypoxia-inducible factor 1 alpha cDNA from chick embryonic ventricular A;Reference number: JCT619; MUID:21134360; PMID:1123772
 A;Content: Embryonic ventricular myocytes
 A;Accession: JCT619
 A;Molecule type: mRNA
 A;Residues: 1-811 <TAK>
 A;Cross-references: DDBJ:AB013746
 C;Comment: This factor belongs to the basic helix-loop-helix-Per/ARNT/Sim (HLH-PAS) family
 C;Genetics:
 A;Gene: hif-1alpha
 C;Keywords: embryo; transcription factor
 P;106-156-/domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS1>
 P;249-299-/domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS2>
 P;762-781-/domain: conserved carboxy-terminal transactivation element #status predicted <PAS3>
 P;767-768/Region: conserved dileucine repeat, important for oxygen-dependent degradation
 Query Match 30.7%; Score 503; DB 2; Length 811;
 Best Local Similarity 49.8%; Pred. No. 8e-36; 72; Indels 28; Gaps 5;
 Matches 119; Conservative 20; Mismatches 36; DB 2; Length 811;
 QY 9 RSNTTELKEKRSRDAARSRSQETEVLYQALHTLPPAREGVSAMLDKASIMRLTISYLRMR 68
 QY 12 RISSERKEKRSRDAARCRRSKESSEVFYELAHOLPLPHTVS AHLDKASIMRLTISYLRMR 71
 QY 69 LCMAGGERGRAT--GRILLPGGGGRHGRHTRRGRGGLPVKCCQARGPQSVDLGSS 123
 Db 72 LLDAGELJETEANNEKEKLNCFYLRKALDSFVMVLSEDG-----DMIVMS 113
 QY 124 LIINNPPTG-TNISLLELICHISIFDPHICPQDQEELQDALTPRPNLSKKLEAPTERHFSIRM 182
 Db 114 ENVINKCMGLTQF-DLTHSISVDPHTPCDHEELRERMLTHRNGEVKKGQEONTERSFLRM 171
 QY 183 KSTLTSRGRTLNIAKATWKLVLICSGHMRAYKPPAQATSPAGSPRSEPPQCLVNLICEAIP 241
 Db 172 KCTLTSRGRTVNIKSATWKLVLICSGHMRAYKPPAQATSPAGSPRSEPPQCLVNLICEAIP 228
 RESULT 3
 138972
 hypoxia-inducible factor 1 alpha - human
 N;Alternate names: ARNT interacting protein
 C;Species: Homo sapiens (man)
 C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C;Accession: I38972; GO1875
 R;Wang, G.L.; Jiang, B.H.; Rue, B.A.; Semenza, G.L.
 Proc. Natl. Acad. Sci. U.S.A. 93: 5510-5514, 1995
 A;Title: Hypoxia-inducible factor 1 is a basic helix-loop-helix-PAS heterodimer regulate
 A;Reference number: 138972; MUID:95296340; PMID:7539918
 A;Accession: I38972
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-826 <RES>
 A;Cross-references: UNIPROT:Q16665; EMBL:U22431; NID:9881345; PID: AAC50152.1; PID:98813
 A;Note: parts of this sequence were confirmed by peptide sequencing
 R;Hogenesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.
 submitted to the EMBL Data Library, June 1995
 A;Reference number: H00692
 A;Accession: GO1875
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-826 <HOG>
 A;Cross-references: EMBL:U29165; NID:91144012; PIDN: AAC51210.1; PID:91144013
 C;Genetics:
 A;Gene: GDB:HIF1A
 A;Cross-references: GDB:512229
 A;Map position: 14q21-14q24
 C;Keywords: heterodimer

best local similarity 46.6%; Freq. No. 4.1e-55; Mismatches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6; Matches 114;

QY 11 NTELRKERKSRAARSRQSQEFLVYQLAHTIIPPARGSALDKASIMRLTISYRMHRIC 70
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 14 SSERRRKERKSRAARSRQSKESEVEYLHQALQPLPWNVSHLKDASMRWLTSYLRVKL 73

Db 71 AAGGKGRATGRLLPSPGGFRHGTTRRGRHGLPVGKQCGQA-----PGVSVDLC 120
 74 DAG-----DLDDEDMGAGMCNCFYIKALGFWVNLTD 105

QY 121 SSSLIH----NPTPG-TNFSLIELTCHSIRPFHCDDEBLQDALTPRNUSKKLEAPT 174
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 106 DGDIMYI1SDNVVKYKMGSLTQF---ELTQHSVFDFTPHCDHEEMRLTHNGLVKKGKEQT 163

QY 175 ERHFSTLRLMKSTLTSRQRTLNKAATWKVHLCGSGHMYAKPAQTSPPASPRSEPPQCLV 234
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 164 QSSPFLAMKCTLTSRQRTLNKAATWKVHLCGSGHMYAKPAQTSPPASPRSEPPQCLV 221

QY 235 LICEAIP 241
 :: :|||:|||:
 Db 222 LICEEPIP 228

RESULT 4

Q4837 hypoxia-inducible factor 1 alpha - mouse

C-Species: Mus musculus (house mouse)

C-Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004

C-Accession: JC4837

R-Wenger, R. H.; Rolfs, A.; Matyi, H. H.; Guenot, J. L.; Gassmann, M. Biochem. Biophys. Res. Commun. 223, 54-59, 1996

A-Title: Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxia-inducible factor 1.

A-Reference number: JC4837; MJD:96254028; PMID:8660378

A-Accession: JC4837

A-Molecule type: mRNA

A-Residues: < 810 < M1N>

A-Cross-references: UNIPROT:Q61221; EMBL:X95580; NID:91430864; PIDN:CAA6833.1; PID:9437

C-Comment: This factor is involved in the oxygen-regulated transcription of several genes.

C-Genetics:

A-Gene: Hif1alpha

A-Map position: 12

C-Keywords: transcription factor

F;5-58/Region: helix-loop-helix #status predicted

Query Match 30.1%; Score 492; DB 2; Length 810;

Best Local Similarity 45.0%; Pred. No. 7.3e-35; Mismatches 112; Conservative 26; Mismatches 59; Indels 52; Gaps 5; Matches 112;

QY 11 NTELRKERKSRAARSRQSQEFLVYQLAHTIIPPARGSALDKASIMRLTISYRMHRIC 70
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 2 SSERRKERKSRAARSRQSKESEVEYLHQALQPLPWNVSHLKDASMRWLTSYLRVKL 61

QY 71 AAGGKGRATGRLLPSPGGFRHGTTRRGRHGLPVGKQCG 113
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 62 DAGGLUSEDDEMKAQMCYFLKALGDGVWVJTDG----- 95

QY 114 POSVDLCSSSLIHNPPTG-TNFSLIELTCHSIRPFHCDDEBLQDALTPRNUSKKLEA 172
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 96 ---DMVYI1SDNVVKYKMGSLTQF---ELTQHSVFDFTPHCDHEEMRLTHNGLVKKGKEQT 149

QY 173 PTERHFSLRLMKSTLTSRQRTLNKAATWKVHLCGSGHMYAKPAQTSPPASPRSEPPQCLV 232
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 150 NTGSPFLAMKCTLTSRQRTLNKAATWKVHLCGSGHMYAKPAQTSPPASPRSEPPQCLV 207

QY 233 LICEAIP 241
 :: :|||:|||:
 Db 208 LVICEEPIP 216

RESULT 5

QCS809 hypoxia-inducible factor 1 alpha - rat

RESULT 8	A29945	184 STUTSRGRTLNKAAATWKLHSGHMR 210 neurogenesis regulatory protein - fruit fly (<i>Drosophila melanogaster</i>) (fragment)	A;Experimental source: clone Y44A6D C;Genetics: C;Species: <i>Drosophila melanogaster</i> C;Accession: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004 A;Reference number: A29945; MUID:88151023; PMID:3345560 A;Accession: A29945 A;Molecule type: mRNA A;Residues: 1-655 <CR> A;Cross-references: UNIPROT: P05709; GB: M19020; NID:9158464; PID:9158465 A;Gene: im A;Cross-references: FlyBase:FBgn0004666 C;Keywords: DNA binding; transcription regulation
Query Match	10.4%	Score 169.5; DB 2;	Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches	62;	Mismatches 90;	Indels 49; Gaps 10;
Query	9 RSNTELKRKSDDAARSRSRSQEVLYQALHTLFA-RGVASHDKAISMLTISYRMH	67	Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Db	4 ELAKLPLPFAITSQSLDKRASVIRLTTSLRMRQVPPDG-LGEAWG---SSPAMQRAI	57	Mismatches 62;
Query	96 HRR-GRRGEL-----PVGKCCQARGPQSVLDCSSLINPPTCINPSLIGHSI	143	Indels 49; Gaps 10;
Db	58 TKELGSHLQITLQGPFIPVAVPAGSKMIVYSETASVHGLS-----QVLTGNIS	105	Matches 62;
Query	144 FFLRIPCTQBLQDALTTRPNLSKKL-----EATI-----ERK 177	174	Best Local Similarity 28.5%; Pred. No. 1.2e-09;
Db	106 PEVIIHNPYQDEMAILSLHPIHNOHPLAQHTPIGSPNGVQHHSAYDPRGSHTIEKT	165	Mismatches 78;
Query	178 FSLRMKSTLTSRGRTLNKAAATWKLHSGHMRAYKPPNQTSPAGSPRSEPPHQCLVNIC	237	Indels 70;
Db	166 FFLRIMKCVLAK--RNAGLTTSGFPRVIIHCSGYLKARYPDRGDG033-----LIONGLVA	218	Gaps 10;
Query	238 -----EAIQPQPFH 246	222	Matches 73;
Db	219 VGHSLPSSAITEIKLH 234	318	Indels 70;
RESULT 9	T21943	hypothetical protein F38A6.3a - <i>Caenorhabditis elegans</i>	A;Experimental source: clone Y44A6D C;Species: <i>Caenorhabditis elegans</i> C;Accession: T21943; T26899 A;Cross-references: UNIPROT:Q9TVM0; EMBL:292833; PIDN: CAB07381.1; GSPDB: GN00023; C
Query Match	10.4%	Score 169.5; DB 2;	Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches	62;	Mismatches 90;	Indels 49; Gaps 10;
Query	9 RSNTELKRKSDDAARSRSRSQEVLYQALHTLFA-RGVASHDKAISMLTISYRMH	67	Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Db	110 KRNMRERTRSHARDRSRSRSQEVLYQALHTLFA-RGVASHDKAISMLTISYRMH	169	Mismatches 62;
Query	68 RLCA---AGGRGRATGRILPEPGGGFRGHGTHRGRHGLPVGKCCQARGPQSVLDCSSL	124	Indels 49; Gaps 10;
Db	170 KTAGVNLLENLDDNEITNEWTET-----TIAECLDG-FVMIIVPSDSSL	212	Matches 62;
Query	125 IHNPTPGTNTFLS---ELIGHISIFPFIHPCDQEQEQLDALTTPRNLSKKLAEPP-----T	174	Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Db	213 YVTESSVAMVGLQITDGLTRGRALRDFLHPSDDEF-----DKOSKMLHKGPRGDTDT	264	Mismatches 62;
Query	175 ERHSLRMKSTLTSRGRTLNKAAATWKLHSGHMRAYKPPAQTSPAG 222	222	Indels 70;
Db	265 GINMVLRMKIVISRGRCNLNSAALKSYSTFVFLYKSVKVRGHSRPMQ-GITIPAG	318	Gaps 10;
RESULT 10	T21944	hypothetical protein F38A6.3b - <i>Caenorhabditis elegans</i>	A;Experimental source: clone Y44A6D C;Species: <i>Caenorhabditis elegans</i> C;Accession: T21944; T26890 A;Cross-references: UNIPROT:Q9TVM0; EMBL:292833; PIDN: CAB07381.1; GSPDB: GN00023; C
Query Match	10.4%	Score 169.5; DB 2;	Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches	62;	Mismatches 90;	Indels 49; Gaps 10;
Query	9 RSNTELKRKSDDAARSRSRSQEVLYQALHTLFA-RGVASHDKAISMLTISYRMH	67	Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Db	110 KRNMRERTRSHARDRSRSRSQEVLYQALHTLFA-RGVASHDKAISMLTISYRMH	169	Mismatches 62;
Query	68 RLCA---AGGRGRATGRILPEPGGGFRGHGTHRGRHGLPVGKCCQARGPQSVLDCSSL	124	Indels 49; Gaps 10;
Db	170 KTAGVNLLENLDDNEITNEWTET-----TIAECLDG-FVMIIVPSDSSL	212	Matches 62;
Query	125 IHNPTPGTNTFLS---ELIGHISIFPFIHPCDQEQEQLDALTTPRNLSKKLAEPP-----T	174	Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Db	213 YVTESSVAMVGLQITDGLTRGRALRDFLHPSDDEF-----DKOSKMLHKGPRGDTDT	264	Mismatches 62;
Query	175 ERHSLRMKSTLTSRGRTLNKAAATWKLHSGHMRAYKPPAQTSPAG 222	222	Indels 70;
Db	265 GINMVLRMKIVISRGRCNLNSAALKSYSTFVFLYKSVKVRGHSRPMQ-GITIPAG	318	Gaps 10;

Db 265 GINMVILRMKTVISPRGRCLNKSALKYKSVFLLVSKVSTGHSVSPMQ-GITIPNG 318
 Qy 16 KEKRDAAARRRSRQETEVLYQALHTPPARGVSAHLKASIMRLTISYLMRHLCAAGK 75
 Db 47 RENHSEIRRERRRNKNTOTIELESDMVPCTCSALARPKPDKLITLVMASHM-----K 96
 Qy 76 RGRATGRILPEPGGGFRICRTHRRGRHGIPLVKGKCOQAPGPOVSDVLCSSLI-HNPTPG 131
 C;Species: Gallus gallus (chicken)
 C;Title: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
 C;Accession: JC7635
 R;Author: T.; Mendiola, M.A.; Smith, S.M.; Born, J.; Walker, M.K.
 Blochim. Biophys. Res. Commun. 282, 602-607, 2001
 A;Title: Hypoxia regulates avian cardiac Arnt and HIF-1alpha mRNA expression.
 A;Reference number: JC7635; MUID:21294777; PMID:11401503
 A;Accession: JC7635
 A;Molecule type: mRNA
 A;Residues: 1-805 <CAT>
 A;Cross-references: UNIPROT:Q98SN3
 C;Comment: This protein, known as hypoxia-inducible factor 1 beta, a member of the basic
 C;Genetics: responses to hormonal and environmental stimuli. It is also a common dimer partner for tran
 A;Gene: arnt1
 C;Keywords: transcription factor
 Query Match 8.7%; Score 142; DB 2; Length 805;
 Best Local Similarity 20.5%; Pred. No. 0.00027;
 Matches 61; Conservative 43; Mismatches 95; Indels 98; Gaps 8;
 Db 89 LARENHSEIRRERRRNKNTOTIELESDMVPCTCSALARPKPDKLITLVMASHM----- 139
 Qy 74 GKRGRATGRILPEPGGGFRICRTHRRGRHGIPLVKGKCOQAPGPOVSDVLCSSLI-HNPT 129
 Db 140 -KSLRGTTGNTSTDGTPKPSLTDQBLKHLI---LEADGFLPIVSCTGRVVRVSDSVT 194
 Qy 130 PGTMF-SLELIGHSTFDIHPCDQEBLQDALTPRPN-----LSKKKLEAPTERHP 178
 Db 195 PVLMQPOQSWFGSTLVDQHPDDPGVKGKLRQQLSTSSENALTEGTPKWCFLSNKDPAPES-- 252
 Qy 179 SLRMKSTLTSRGRTANKAAATW----- 201
 Db 253 -----ASKGRIDLKIGTIVKKEGQQSKRMRMCGSRRSFICRMRCCGNSSDAVSNRLS 304
 Qy 202 -----VLLCSGHRAKYKPAQISPGSP-RSEEPQLCVLI 236
 Db 305 FMRMRCRNGLGATKDGEPHYVVFHCTGYIKAWPPAGVSLPDDPDAGQSKFCFLVAI 361
 RESULT 12
 JC7633 aryl hydrocarbon nuclear translocator ARNT2-like factor, ARNT2X - zebra fish
 C;Species: Brachydanio rerio (zebra fish)
 C;Title: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
 C;Accession: JC7633
 R;Hsu, H.J.; Wang, W.D.; Hu, C.H.
 Blochim. Biophys. Res. Commun. 282, 487-492, 2001
 A;Title: Ecotypic expression of negative ARNT2 factor disrupts fish development.
 A;Reference number: JC7633; MUID:21294759; PMID:11401485
 A;Contents: Heart
 A;Accession: JC7633
 A;Molecule type: mRNA
 A;Residues: 1-392 <HSU>
 A;Cross-references: UNIPROT:Q98SK3; GB:AY007992
 C;Comment: This factor, a basic helix-loop-helix PAS (bHLH-PAS) factor, heterodimerizes
 C;Genetics:
 A;Gene: arnt2X
 Query Match 8.5%; Score 138.5; DB 2; Length 392;
 Best Local Similarity 20.8%; Pred. No. 0.00023;
 Matches 55; Conservative 48; Mismatches 103; Indels 59; Gaps 8;

Db 55448 Ar receptor nuclear translocator - mouse
 C;Species: Mus musculus (house mouse)
 C;Title: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
 C;Accession: A55448
 RESULT 14
 Db 97 SMRGTTGNTSTDGAYKPSLTDQBLKHLI---LEADGFLPIVSCTGRVVIYSDSVT 152
 Qy 132 TNF-SLELIGHSTFDIHPCDQEBLQDALTPRPN-----LNKAAATKVLKSGHMDY 212
 Db 153 LNHRQSEWFGSTLFEQVHDVVKLREQLSTSNSMTRGKLDLKTGTWKEGQSSMMRC 212
 Qy 171 -----RAPHRHSFLRMKSTLTSRGRT---LNKAAATKVLKSGHMDY 212
 Db 213 MGSRSPFCRMRCGSAAPD-HISLNRLSSMTRKRYNGLGPSSKEGAQSVWHTGYIWA 271
 Qy 213 KPPAQTSR-AGSPRSEPPHQCLVLI 236
 Db 272 PPAGMTIPDEDTEAQTSKYLVAI 296
 RESULT 13
 A56241 aryl hydrocarbon receptor nuclear translocator protein - mouse
 C;Species: Mus musculus (house mouse)
 C;Title: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C;Accession: A56241
 R;Reis-Perez, S.; Probst, M.R.; Fukunaga, B.N.; Hankinson, O.
 Mol. Cell. Biol. 14, 6075-6086, 1994
 A;Title: Identification of functional domains of the aryl hydrocarbon receptor nuclear t:
 A;Reference number: A56241; MUID:94344118; PMID:8065341
 A;Accession: A56241
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-791 <REI>
 A;Cross-references: UNIPROT:P53162; GB:U00325; NID:9555687; PID:AAA56717.1; PID:9555668
 A;Note: authors translated the codon TTT for residue 375 as Ser, TCT for residue 380 as C
 A;Note: authors failed to translate CAG for residue 507 as Gln
 C;Genetics:
 A;Gene: ARNT
 Query Match 8.5%; Score 138.5; DB 2; Length 791;
 Best Local Similarity 21.8%; Pred. No. 0.00053;
 Matches 58; Conservative 50; Mismatches 101; Indels 57; Gaps 9;
 Db 89 LARENHSEIRRERRRNKNTOTIELESDMVPCTCSALARPKPDKLITLVMASHM----- 139
 Qy 140 -KSLRGTTGNTSTDGAYKPSLTDQBLKHLI---LEADGFLPIVSCTGRVVIYSDSVT 194
 Db 74 GKRGRATGRILPEPGGGFRICRTHRRGRHGIPLVKGKCOQAPGPOVSDVLCSSLI-HNPT 129
 Db 140 -KSLRGTTGNTSTDGAYKPSLTDQBLKHLI---LEADGFLPIVSCTGRVVIYSDSVT 194
 Qy 130 PGTMF-SLELIGHSTFDIHPCDQEBLQDALTPRPN-----LSKKKLEAPTE 174
 Db 195 PVLMQPOQSWFGSTLVDQHPDDPGVKGKLRQQLSTSSENALTEGTPKWCFLSNKDPAPES-- 254
 Qy 175 -----ERFLSKMSTL-----KGRTANKAAAT-----WKLHCSHMR 211
 Db 255 MCMGSSRRSFICRMRCCGTSVSDVPSMNRNISFLRNCRNGLGSVKEGPFFVVFHCTGYIKA 314
 Qy 212 YKPPAQTSR-AGSPRSEPPHQCLVLI 236
 Db 315 WPPAGVSLPDDPDEAGQSKFCFLVAI 340

R.Li, H.; Dong, L.; Whitlock Jr., J.P.
J. Biol. Chem. 269, 28098-28105, 1994

A:Tittle: Transcriptional activation function of the mouse Ah receptor nuclear translocator

A:Reference number: A55448; MUID:95050586; PMID:7961746

A:Accession: A55448

A:Status: preliminary

A:Residue: 1-176 <LIA>

A:Cross-references: UNIPROT:Q921F3; GB:U14333

Query Match 8.3%; Score 136.5; DB 2; Length 776;
Best Local Similarity 21.2%; Pred. No. 0.00077; Mismatches 109; Indels 57; Gaps 9;
Matches 58; Conservative 50; MisMatches 109; Indels 57; Gaps 9;

Qy 6 QVRNSNTLRLKEKERAARSRSRQSOETEVILQLAHTLPPARGVSAHLDKASIMRLTISVL 65
Db 66 QMCNDKDERARENHESEIERRRRNQNTAVITELSPMVPCTSCALARPKDPLTURMVAHM- 124
Qy 66 MHRILCAAGGKRRGRATGRGLLPEGRGPRHGRHGLPVGKQOAPRQFSDICSSLI 125
Db 125 - - - - - KSLRGITGNTSTDGSYKPSFLTDQELKHLI- - - - - LIAADGFLFTVSCETGRV 171
Qy 126 - - - - - HNPPTPGTNF-SLELIGHSTIFDFIIRCDQEBLQDALITPREN-LSEKKLEAPT- - - - 174
Db 172 VVYSDSVTPVLNQPOSEWFGSTLYDQVHPPDDVQKREOLUSTSENALTGRVLDLKTGTVK 231
Qy 175 - - - - - ERHFSLRLMKSILS- - - - - RGRITNLKAT- - - - - WKVL 203
Db 232 EGQQQSSMRMOMGSRSPICRMCCTSYDPSMNRSLFLRNRCNGLGSVKGSEPHFVV 291
Qy 204 HCSHMRAVKPAAOTSPAGSPRS-EPPLOCLVLI 236
Db 292 HCTGYIKAWPPAGVSLPDDPEAQGQSKFCLVAI 325

RESULT 15

159550 aryl hydrocarbon receptor nuclear translocator Arnt [imported] - human

C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004C:Accession: 159550
R:Hoffman, E. C.; Reyes, H.; Chu, F.F.; Sander, P.; Conley, L.H.; Brooks, B.A.; Hankinson, Science 252, 954-958, 1991
A:Tittle: Cloning of a factor required for activity of the Ah (dioxin) receptor.

A:Reference number: 159550; MUID:91240280; PMID:1852076

A:Accession: 159550

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Residue: 1-1789 <RES>

A:Cross-references: UNIPROT:P27540; GB:M69238; NID:9179003; PID:AAA51777.1; PID:9179004

C:Genetic

A:Gene: GDB:ARNT

A:Cross-references: GDB:119701; OMIM:126110

A:Map position: 1q21-1q21

Query Match 8.3%; Score 136.5; DB 2; Length 789;
Best Local Similarity 21.8%; Pred. No. 0.00079; Mismatches 101; Indels 57; Gaps 9;
Matches 58; Conservative 50; MisMatches 101; Indels 57; Gaps 9;

Qy 14 LRKKEKSDAARSRSRQSOETEVILQLAHTLPPARGVSAHLDKASIMRLTISVLHRLCAG 73
Db 89 LARENHSSEIERRRRNQNTAVITELSPMVPCTSCALARPKDPLTURMVAHM- 139
Qy 74 KGRGATGTRGIPGGGGFRHGRGRGLPVGKQQAPGQPSVDCSSSLI- - - - - HNPT 129
Db 140 - - - - - KSLRGITGNTSTDGSYKPSFLTDQELKHLI- - - - - LIAADGFLFTVSCETGRV 194
Qy 130 PGTFNP-SLELIGHSTIFDFIIRCDQEBLQDALITPREN-LSEKKLEAPT- - - - - 174
Db 195 PVLNQPOSEWFGSTIYDQVHPPDDVQKREQLSISENALITGRILDLKIGTVKKGQOSSMR 254
Qy 175 - - - - - ERHFSLRLMKSILS- - - - - RGRITNLKAT- - - - - WKVLHSGMRA 211

Do 255 MCNGSRSFICMRCCSSSVDPVSNRSCRNGLGSVKGDFPFWVHCTGYIKA 314
Qy 212 YKPAQTSPPASPRS-EPLQLCIVLI 236
Do 315 WPPAGVSLPDDPAGQGSKFCLVAI 340

Search completed: June 15, 2005, 16:00:54
Job time : 42 secs

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Q89gm4 fundulus heteroclitus

Q63161 xenopus laevis

Q9W7C6 gallus gallus

Q9tb3 coturnix coqui

Q9Kta4 bos taurus

Q9814 homo sapiens

Q5P97 xenopus laevis

Q65912 xenopus laevis

Q918w2 oncorhynchus tshawytscha

Q917z9 homo sapiens

Q6ryc8 ovis aries

Q6ryc9 sus scrofa

Q84d6 mus musculus

Q7t2e4 brachydanio

Scoring table:		BLOSUM62										Gapop 10.0 , Gapext 0.5									
Searched:		1612378 seqs, 512079187 residues										1612378									
Total number of hits satisfying chosen parameters:		1612378										1612378									
Minimum DB seq length: 0		AC										AC									
Maximum DB seq length: 2000000000		DT										DT									
Post-processing:		Minimum Match 0%										DT									
Maximum Match 100%		DT										DT									
Listing first 45 summaries		01-MAR-2002 (TREMblrel. 20, Last sequence update)										01-MAR-2004 (TREMblrel. 26, Last annotation update)									
Database :		UniProt_03;*										Name=HiF3a; Synonyms=tpas;									
1: uniprot_sprot:*		OS										Mus musculus (Mouse).									
2: uniprot_trembl:*		OC										Bularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		RN										NCBI_TaxID=10090;									
SUMMARIES		RP										SEQUENCE FROM N.A.									
Result No.		RC										STRAIN=C57BL/6J; PubMed=11734056; DOI=10.1038/35107085; RXN									
Score		RA										RA									
Query		RC										RA									
Match		RC										RA									
Length		RC										RA									
DB		RC										RA									
ID		RC										RA									
Description		RESULT 1										RESULT 1									
		Q8VHR1										Q8VHR1									
		PRELIMINARY;										PRELIMINARY;									
		PRT;										PRT;									
		307 AA.										307 AA.									
		1612378										1612378									
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		1612378</td																			

QY	121 -----SSLLIHNPTGPNPS-LELIGHSIFDRIHPCDQEELQDALTRPRPNLSSKKL 170	RESULT 5
Db	95 WVVLLTAEGDVAAYLSENVKHNKGQLSPELIGHSIFDRIHPCDQEELQDALTRPRNPKKL 154	Q66K72 PRELIMINARY; PRT; 669 AA.
QY	171 BAPTERHFSLMMKSTLTSRGRTLNKATATWKLVLHCSGHMRAVKPPQTSPGSPRSEPL 230	ID Q66K72; PRELIMINARY; PRT; 669 AA.
Db	155 BAPTERHFSLMMKSTLTSRGRTLNKATATWKLVLHCSGHMRAVKPPQTSPGSPRSEPL 214	AC Q66K72; PRELIMINARY; PRT; 669 AA.
QY	231 QCLVILICEAIP----QLPFDGATL 251	DT 25-OCT-2004 (TREMBIrel. 28, Last sequence update)
Db	215 QCLVILICEAIP----QLPFDGATL 240	DT 25-OCT-2004 (TREMBIrel. 28, Last annotation update)
RESULT 4		
Q8WZL1	PRELIMINARY; PRT; 632 AA.	DE HIF3A protein.
AC		GN Name=HIFRA;
DT	01-MAR-2002 (TREMBIrel. 20, Created)	OS Homo sapiens (Human).
DT	01-MAR-2004 (TREMBIrel. 26, Last annotation update)	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buterria; Primates; Catarrhini; Hominidae; Homo.
RN	[1]	OC NCBI_TaxID=9606;
RP	SEQUENCE FROM N.A.	RN
RL	Submitted (DEG-2001) to the EMBL/GenBank/DBJ databases.	RP SEQUENCE FROM N.A.
CC	!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.	RC TISSUE=Pancreas;
DR	EMBL: AF063492; AAU99497.1; -.	RA Published=1247932; DOI=10.1073/pnas.242603899;
DR	HSSP: Q16665; I1QB.	RA Strasserberg R.D., Feingold E.A., Wagner L., Shamen C.M., Schuler G.D., Klausner R.D., Collins P.S., Wagner L., Shamen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Udin T.B., Toshimori S., Cabanac R., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaway S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Munoz D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Heiton B., Kettelman M., Madan A., Rodriguez S., Sanchez A., Raya M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.J., Schmitz J.J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska D.E., Schein J.E., Jones S.J., Marr M.A.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
DR	GO: GO:0003700; F-transcription factor activity; IEA.	RA
DR	GO: GO:000535; Regulation of transcription, DNA-dependent; IEA.	RA
DR	GO: GO:000165; P:signal transduction; IEA.	RA
DR	GO: GO:0004871; F:signal transducer activity; IEA.	RA
DR	Pfam: PF00010; HLH; 1.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
DR	SMART; SNO0086; PAC; 1.	RA
DR	SMART; SNO0091; PAS; 2.	RA
DR	PROSITE; PS50112; PAS; 2.	RA
DR	PFam; PF00099; PAS; 1.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
DR	SMART; SNO0091; PAS; 2.	RA
DR	PROSITE; PS50112; PAS; 2.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
DR	SMART; SNO0091; PAS; 2.	RA
DR	PROSITE; PS50112; PAS; 2.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
DR	SMART; SNO0091; PAS; 2.	RA
DR	PROSITE; PS50112; PAS; 2.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
DR	SMART; SNO0091; PAS; 2.	RA
DR	PROSITE; PS50112; PAS; 2.	RA
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DR	PRINTS; PR00785; NCTNSLOCATR.	RA
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DR	PROSITE; PS50112; PAS; 2.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
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DR	PRINTS; PR00785; NCTNSLOCATR.	RA
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DR	PROSITE; PS50112; PAS; 2.	RA
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DR	PROSITE; PS50112; PAS; 2.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
DR	SMART; SNO0091; PAS; 2.	RA
DR	PROSITE; PS50112; PAS; 2.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
DR	SMART; SNO0091; PAS; 2.	RA
DR	PROSITE; PS50112; PAS; 2.	RA
DR	PRINTS; PR00785; NCTNSLOCATR.	RA
DR	SMART; SNO0353; HLH; 1.	RA
DR	SMART; SNO0091; PAS; 2.	RA
DR	PROSITE; PS50112; PAS; 2.	RA
DR		

QY	229	PLQCVLICBAIPOLPFHGA	249	Query Match 50.8%; Score 831; DB 2; Length 632;
Db	215	PLQCVLICBAIP---HPGS	231	Best Local Similarity 68.2%; Pred. No. 26-60; Mismatches 30; Indels 42; Gaps 5; Matches 178; Conservative 11; Mismatches 30; Indels 42; Gaps 5;
RESULT 6				
ID	Q96K34	PRELIMINARY;	PRT;	632 AA.
AC	Q96K34;			
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBrel. 26, Last annotation update)			
DE	Hypothetical protein FLJ14819.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary; DOI=10.1038/ng1285; PubMed=14720339;			
RX	RA			
RA	Ota T., Suzuki Y., Nisikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi T., Kawai Y., Isono Y., Isomura Y., Nakamura Y., Nagahashi K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoi T., Kaku Y., Kocaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoji Y., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Saito K., Tanikawa M., Yamazaki M., Niimura K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa M., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotota T., Kubano J., Kamehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togoya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunaga H., Ichihara T., Shiohara N., Sano S., Moriya S., Momiyama H., Satoh S., Takanishi Y., Terashima Y., Suzuki O., Nagagawa S., Seroh A., Mizoguchi H., Gotto Y., Shimizu P., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., RA			
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y., Kawabata A., Hikiji T., Kobatake H., Imagai Y., Ikeda Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsunaga K., Nakemura Y., Mizuno T., Morinaga M., Komatsu T., Komatsu M., Hata H., Watanabe T., Shirai Y., Takahashi Y., Nakagawa K., Misushima-Sugano J., Satoh T., Nakamura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara S., Isogai T., Sugano S., Nakai K., Yada T., Nakamura Y., Ohara S., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human RT cDNAs."; RT Nat. Genet. 36:40-45 (2004).			
RT	RT			
CC	-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.			
DR	EMBL; AK027725; BAB55324.1; -; HSPB; Q9P814; 1P97.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:000871; F:signal transducer activity; IEA.			
DR	GO; GO:0003700; F:transcription factor activity; IEA.			
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	GO; GO:0007165; P:signal transduction, IEA.			
DR	GO; GO:0007165; P:signal transduction, IEA.			
DR	GO; GO:0005334; C:nucleus; IEA.			
DR	GO; GO:0003701; F:signal transducer activity; IEA.			
DR	GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.			
DR	GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.			
DR	GO; GO:0007165; P:signal transduction, IEA.			
DR	GO; GO:0007165; P:signal transduction, IEA.			
DR	InterPro; IPR01092; HUH basic.			
DR	InterPro; IPR00167; Nuc_translocat.			
DR	InterPro; IPR00160; PAC.			
DR	InterPro; IPR00014; PAS.			
DR	Pfam; PF00010; HUH; 1.			
DR	Pfam; PF00999; PAS; 1.			
DR	PRINTS; PR00785; NCTRNLSLOCATR.			
DR	SMART; SM00533; HUH; 1.			
DR	SMART; SM00066; PAC; 1.			
DR	SMART; SM00091; PAS; 2.			
DR	PROSITE; PS50112; PAS; 2.			
DR	PROSITE; PS50112; PAS; 2.			
SQ	SEQUENCE 662 AA; 72887 MW; AC9572E340544010 CRC64;			
	Query Match 50.2%; Score 820.5; DB 2; Length 662;			
	Best Local Similarity 68.1%; Pred. No. 1 6e-59; Matches 177; Conservative 9; Mismatches 31; Indels 43; Gaps 5;			

7 RSTBLRKEKSRDAARSRSQETEVLYQAHTRPARGVSAAHDKASIMRLTISYRMR 66
 69 LCAAGGKGRATGRULPEPGGFRHGTHRGHGLPVGKQO-----QAPGPOSV 117
 67 LCAAG-----EWNOVKEEPLACYLKALEGFVNVLTAEGDMAY 106
 118 DLCCSSLINHPTPGNFS LEHIGHSIFDPHPCDQEELQDALTPRPNLSKKLEAPTER 176
 107 -----LSENVSKHGLSQUELIGHTSIFDPHPCDQEELQDALTPRPLSKGSEATCR 160
 177 HFSLRMKSTTSRGETNLNKAATKWLHSGHMRAYKPPAQTSAGSPRSPEPQCLVLI 236
 161 HFSLRMKSTTSRGETNLNKAATKWLHSGHMRAYKPPAQTSAGSPRSPEPQCLVLI 220
 237 CEATIP-----OLPFDGATL 251
 221 CEATIPHSASIEPPGLGGAFL 240

RESULT 8

Q9Y2N7 PRELIMINARY; PRT; 667 AA.
 ID Q9Y2N7; AC 09Y2N7; DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative homolog of hypoxia inducible factor three alpha (Hypoxia-inducible factor-3 alpha).
 DR Name=HIF-3A;
 OS Homo sapiens (Human);
 OC Bulyryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606; RN [1]

SEQUENCE FROM N.A.

RA Lamerdin J.B., McReady P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry J., Barnes J., Liu S.,
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas P., Bruce P., Quan G., Kronmiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.,
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]

SEQUENCE FROM N.A.

RP TISSUE=kidney;

RX MEDLINE=21450277; PubMed=11573933; DOI=10.1007/bfrc.2001.5659;
 RA "Expression and characterization of hypoxia-inducible factor (HIF)-1alpha in human kidney: suppression of HIF-mediated gene expression by HIF-3alpha.",
 RA Blochman. *Biophys. Res. Commun.* 287:808-813(2001).
 CC -- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL: AC001193; AND2668.1; -.
 DR EMBL: AB054067; BAB69689.1; -.
 DR PIR: JCT771; JCT771.
 DR HSSP: Q16665; 1LQB.
 DR GeneID: HGNC:5825; HIF3A.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0004871; P:signaling transducer activity; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO: GO:0007165; P:signaling transduction; IEA.
 DR InterPro: IPR01052; HIF_basic.
 DR InterPro: IPR01067; Nuc_translocat.
 DR InterPro: IPR001610; PAC.
 DR InterPro: IPR00014; PAS.
 DR Pfam: PF00989; PAS; 1.
 DR PRINTS; PR00785; NCTRNLSLOCATR.
 SMART; SMO0353; HIFH; 1.
 Okumura K., Nagase T., Nomura N., Kiruchi H., Masuho Y., Yamashita R.,

DR SMART; SM00086; PAC; 1.
 DR SMART; SM00031; PAS; 2.
 DR PROSITE; PS00112; PAS; 2.
 DR SEQUENCE; 667 AA; 72404 MN; 67B8794FF9DCCF4B CRC64;

Query Match 49.0%; Score 802; DB 2; Length 657; Best local similarity 68.0%; Pred. No. 5.5e-58; Indels 42; Gaps 5; Matches 172; Conservative 11; Mismatches 28; DR
 9 RSTBLRKEKSRDAARSRSQETEVLYQAHTRPARGVSAAHDKASIMRLTISYRMR 68
 7 RSTBLRKEKSRDAARSRSQETEVLYQAHTRPARGVSAAHDKASIMRLTISYRMR 66
 177 HFSLRMKSTTSRGETNLNKAATKWLHSGHMRAYKPPAQTSAGSPRSPEPQCLVLI 236
 161 HFSLRMKSTTSRGETNLNKAATKWLHSGHMRAYKPPAQTSAGSPRSPEPQCLVLI 220
 237 CEATIP-----OLPFDGATL 249
 221 CEATIPHSASIEPPGLGGAFL 229

RESULT 9

Q9HAI2 PRELIMINARY; PRT; 648 AA.
 ID Q9HAI2; AC 09HAI2; DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Hypothetical Protein FLJ1591.
 OS Homo sapiens (Human).
 OC Bulyryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606; RN [1]

SEQUENCE FROM N.A.

RP TISSUE=whole embryo;

RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahori K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Watanabe M., Shiratori A.,
 RA Sudo H., Hosozaki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niromiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hidaka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotoda T., Kusano J.,
 RA Kaneko K., Takahashi-T Fujii R., Hara H., Tanase T., Nomura Y.,
 RA Togita S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Murashimo K., Yuki H., Oshima A., Sasaki N., Notsuka S.,
 RA Yoshikawa Y., Makunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Shimizu Y., Suzuki O.,
 RA Nakagawa S., Senon A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe A., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Iitema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senna T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Ogawa M., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakashawa K.,
 RA Okumura K., Nagase T., Nomura N., Kiruchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RL Nat. Genet. 36:40-45 (2004).
 DR EMBL; ARK021653; BAB13865.1; -.
 DR HSSP; Q16665; 1LQB.
 DR GO; GO:0004871; P:signal transducer activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:000765; P:signal transduction; IEA.
 DR InterPro; IPR001610; PAC.
 DR Pfam; PF00989; PAS; 1.
 DR SMART; SMD0031; PAS; 2.
 DR PROSITE; PS50112; PAS; 2.
 RA SEQUENCE 648 AA; 69995 MN; BBBFC744BC3F148B CRC64;
 Query Match 35.0%; Score 573; DB 2; Length 648;
 Best Local Similarity 61.0%; Pred. No. 5, 45-39;
 Matches 125; Conservative 11; Mismatches 27; Indels 42; Gaps 5;
 QY 57 MRLTISYLRHLCAAGGKGKGATGRGLRPGPGFRRGHGTHRGRGLPVGKQ----- 109
 1 MULTISYLRHLCAAGGKGKGATGRGLRPGPGFRRGHGTHRGRGLPVGKQ----- 109
 Db 41 VMVLTAEQGDMAY-----LSENVSKHIGLSQLLELGHSTFDIHPDCDBEQLDALTPOQ 94
 QY 165 LSKKCLEAFTERHSLRMGSTLSRGRTNLKATWKVHLCSGHMRKAKPPOTSPPGSP 224
 95 LSRRKVEAFTERHSLRMGSTLSRGRTNLKATWKVHLCSGHMRKAKPPOTSPPGSP 154
 QY 225 RSEPPQCLVCLICAIPOLPFHGDA 249
 155 DSEPPQCLVCLICAIPOLPFHGDA 249
 Db SEQUENCE 199 AA; 21598 MN; 646CB066A09B47C3 CRC64;
 Query Match 31.7%; Score 518.5; DB 2; Length 199;
 Best Local Similarity 68.0%; Pred. No. 4, 5e-35;
 Matches 104; Conservative 9; Mismatches 13; Indels 27; Gaps 2;
 QY 120 CSSSLIRHPTPGINP-----SLELGHISFFIHPDCDBEQLQ 156
 14 CTSWLTRCPSPASAPWTPRLSCASPSATCACTASARQLELGHISFFIHPDCDBEQLQ 73
 Db 157 DALTPRPNLSKKEAFTERHSLRMGSTLSRGRTNLKATWKVHLCSGHMRKAKPPA 216
 74 DALTPQQTLSRKKVEAFTERHSLRMGSTLSRGRTNLKATWKVHLCSGHMRKAKPPA 133
 QY 217 QTPSPAGSRSEPPQCLVCLICAIPOLPFHGDA 249
 Db 134 QTPSPAGSDSEPPQCLVCLICAIPOLPFHGDA 162
 RESULT 11
 HIF1A_CHICK ID HIF1A_CHICK STANDARD; PRT; 811 AA.
 AC QWV¹B; DT 10-OCT-2003 (Rel. 42, Created)
 ID QHAMS5; PRELIMINARY; PRT; 199 AA.
 DT 01-MAR-2001 (Trembl; 16, Last sequence update)
 DT 01-OCT-2002 (Trembl; 22, Last annotation update)
 DE Hypothetical protein FLJ11359.
 OS Homo sapiens (Human).
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI - TaxID:9606;
 OC NCBI - TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole embryo.
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Otsubi T., Suzuki Y., Nishikawa T., Otsubi T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi M., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Isaji S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Waga T., Shiratori A.,
 RA Sudo H., Hosocri T., Koku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niomiyama K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoida M., Hotuta T., Kusano J.,
 RA Kaneko K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togia S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Murashino K., Yuuki H., Oshima A., Sakaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriy S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamasaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujisawa T.,
 RA Ono T., Yamada K., Fujii Y., Okaji K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inabaki H., Ikeda Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Sato T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagae T., Nomura N., Kikkuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 CONDA";
 RL Nat. Genet. 36:40-45 (2004).
 DR EMBL; ARK021421; BAB13819.1; -.
 DR SMART; Q9814; 1997.
 DR PROSITE; PS50112; PAS; 2.
 RA SEQUENCE 199 AA; 21598 MN; 646CB066A09B47C3 CRC64;
 Query Match 31.7%; Score 518.5; DB 2; Length 199;
 Best Local Similarity 68.0%; Pred. No. 4, 5e-35;
 Matches 104; Conservative 9; Mismatches 13; Indels 27; Gaps 2;
 QY 120 CSSSLIRHPTPGINP-----SLELGHISFFIHPDCDBEQLQ 156
 14 CTSWLTRCPSPASAPWTPRLSCASPSATCACTASARQLELGHISFFIHPDCDBEQLQ 73
 Db 157 DALTPRPNLSKKEAFTERHSLRMGSTLSRGRTNLKATWKVHLCSGHMRKAKPPA 216
 74 DALTPQQTLSRKKVEAFTERHSLRMGSTLSRGRTNLKATWKVHLCSGHMRKAKPPA 133
 QY 217 QTPSPAGSRSEPPQCLVCLICAIPOLPFHGDA 249
 Db 134 QTPSPAGSDSEPPQCLVCLICAIPOLPFHGDA 162
 RESULT 12
 HIF1A_CHICK ID HIF1A_CHICK STANDARD; PRT; 811 AA.
 AC QWV¹B; DT 10-OCT-2003 (Rel. 42, Last sequence update)
 ID QHAMS5; PRELIMINARY; PRT; 199 AA.
 DT 01-MAR-2001 (Trembl; 16, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
 GN Name=HIF1A;
 OS Gallus Gallus (Chicken).
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosuria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus
 OC NCBI - TaxID:9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Takahashi T.;
 RT "Molecular cloning and expression of an avian cDNA for hypoxia-
 RT inducible factor-1 alpha in embryonic ventricular myocytes.";
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
 CC -1 FUNCTION: Functions as a master transcriptional regulator of the
 CC additive response to hypoxia. Binds to core DNA sequence 5'-
 CC [AGTCGCG-3', within the hypoxia response element (HRE) of target
 CC gene promoters. Activation requires recruitment of transcriptional
 CC coactivators (By similarity).
 CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an
 CC alpha and a beta/ARNT subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cyttoplasmic in normoxia; nuclear
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC

DR EMBL; AB013746; BAA34234.2; -.

DR HSSP; Q16655; IHX.

DR InterPro; IPR001092; HLU basic.

DR InterPro; IPR001321; HypoxindlFA.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLU; 1.

DR Pfam; PF0075; PAC; 1.

DR Pfam; PF00989; PAS; 2.

DR PRINTS; PR01080; HYPOXIAIFIA.

DR SMART; SM00353; HLU; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM0091; PAS; 2.

DR PROSITE; PS5088; HLU; 1.

DR PROSITE; PS50112; PAS; 2.

KW Activator; DNA-binding; Nuclear protein; Repeat;

KW Transcription regulation.

FT DNA_BIND 17 30 Basic motif.

FT DOMAIN 31 71 Helix-loop-helix motif.

FT DOMAIN 80 157 PAS 1.

FT DOMAIN 228 298 PAS 2.

FT DOMAIN 302 345 PAC.

FT DOMAIN 401 587 ODD.

FT DOMAIN 529 573 NTAD.

FT DOMAIN 576 705 ID.

FT DOMAIN 703 706 Nuclear localization signal (Potential).

FT DOMAIN 718 721 Nuclear localization signal (Potential).

FT DOMAIN 771 811 CTAD.

FT DOMAIN 583 588 Poly-Ser.

SQ SEQUENCE 811 AA; 90542 MW; D4CD9F98F064CB CRC64;

Query Match 30.7%; Score 503; DB 1; Length 811;
Best Local Similarity 49.8%; Fred. No. 4.6e-33;
Matches 119; Conservative 20; Mismatches 72; Gaps 5;

QY 9 RNTLRLKEKNSDAARSRSRSQSETENYQQLAHTLPFARGVSAHLKASIMRLTISYLRMR 68

12 RISSRKRKERSDAARCRRSSESEYFELAHQPLRHTVSAHLKASIMRLTISYLRMR 71

QY 69 LCAAGGKGKRGAT----GRUPEGGPGRGTHRGKRGHGPVGKQQAQGPPOSTDCESS 123

Db 72 LDDABELETANMNEKLNCLYKALDGFVWNLSEBDG-----DMIVMS 113

QY 124 LIHAPTPG-TNFSLELGHISFDFIHPHQELQDQLALTRPRNLSKKKLRPTEHPSLRL 182

114 ENVKOMGLTOP--DLTGHSVDFTHPCDHEELRMLTHNGPVTKGKESQNTBRSFFLM 171

QY 183 KSTLTSRGRTNLKATWKVHLCSCHMRAYRPPACTSPACGSPRSRBPPLQCLVILCEAIP 241

Db 172 KCTUTSRGRTNVIKSATWKVHLCTGHIRVYDTCNNQTHCG--YKKPPMTCLVILCEPIP 228

RESULT 12

HIF1A_BOVIN STANDARD; PRT; 823 AA.

ID HIF1A_BOVIN STANDARD; PRT; 823 AA.

AC 0X9TA5;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DB Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).

GN Name=HIF1A;

OS Bos taurus (Bovine).

OC Nukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos;

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Artery;

RC MEDLINE=9255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;

RA Hara S.; Kobayashi C.; Imura N.;

RA "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF) -1 and -2 in bovine arterial endothelial cells.",

RA Ialha and -2alpha of bovine arterial endothelial cells.",

RL Biochim. Biophys. Acta 1445:237-243 (1999).

CC -1- FUNCTION: Functions as a master transcriptional regulator of the adaptive response to hypoxia. Under hypoxic conditions activates the transcription of over 40 genes, including, erythropoietin, glucose transporters, glycolytic enzymes, vascular endothelial growth factor, and other genes whose protein products increase oxygen delivery or facilitate metabolic adaptation to hypoxia. Plays an essential role in embryonic vascularization, tumor angiogenesis and pathophysiology of ischemic disease. Binds to core DNA sequence 5'-[AG]CTG-3', within the hypoxia response element (HRE) of target gene promoters. Activation requires recruitment of transcriptional coactivators such as CREBPP and CREBPP (By similarity).

CC -1- SUBUNIT: Efficient DNA binding requires heterodimerization of an alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of CREBPP and EP300. Interacts with NCOA1, NCOA2, APEX and Hsp90 (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear translocation in response to hypoxia (By similarity).

CC -1- DOMAIN: Contains two independent C-terminal transactivation domains, NTAD and CTAD, which function synergistically. Their transcriptional activity is repressed by an intervening inhibitory domain (ID) (By similarity).

CC -1- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-564 in the oxygen-dependent degradation domain (ODD) by EGLN1/PRO1 and EGLN2/PHD3. EGLN3/PHD3 has also been shown to hydroxylate Pro-564. The hydroxylated prolines promote interaction with VHL, initiating rapid ubiquitination and subsequent proteasomal degradation. Under hypoxia, proline hydroxylation is impaired and ubiquitination is attenuated, resulting in stabilization (By similarity).

CC -1- PTM: In normoxia, is hydroxylated on Asn-800 by HIF1AN, thus abbreviating interaction with CREBPP and EP300 and preventing transcriptional activation (By similarity).

CC -1- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-nitrosylation in vitro, however not all thiol groups seem to be nitrosylated in vivo (By similarity).

CC -1- PTM: Acetylation of Lys-532 by APL increases interaction with VHL and stimulates subsequent proteasomal degradation (By similarity).

CC -1- PTM: Requires phosphorylation for DNA-binding (By similarity).

CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

CC

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CC

DR EMBL; AB018298; BRA78675.1; -.

DR HSSP; Q16655; 1BC.

DR InterPro; IPR001092; HLU basic.

DR InterPro; IPR001321; HypoxindlFA.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLU; 1.

DR Pfam; PF0075; PAC; 1.

DR Pfam; PF00989; PAS; 2.

DR PRINTS; PR01080; HYPOXIAIFIA.

DR SMART; SM00353; HLU; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM0091; PAS; 2.

RL	Biochem. J. 354:531-537(2001).	DR	Pfam; PF00010; HhH; 1.
RN	[2]	DR	Pfam; PF00785; PAC; 1.
RP	SEQUENCE FROM N.A.	DR	Pfam; PF00989; PAS; 2.
RC	STRAIN=Sprague-Dawley; TISSUE=Kidney;	PRINTS	PRO1080; HYPOXIAIFIA.
RX	MEDLINE=21417706; PubMed=11526200;	SMART	SM00353; HhH; 1.
RA	ZOU, A.-P., Yang, Z.-Z., Li, P.-L., Cowley, A.W. Jr.;	DR	SMART; SM0086; PAC; 1.
RT	"Oxygen-dependent expression of hypoxia-inducible factor-1alpha in renal medullary cells of rats";	SMART	SM0091; PAS; 2.
RL	Physiol. Genomics 6:155-168(2001).	DR	PROSITE; PSS0888; HhH; 1.
CC	-!- FUNCTION: Functions as a master transcriptional regulator of the adaptive response to hypoxia. Under hypoxic conditions activates the transcription of over 40 genes, including, erythropoietin, glucose transporters, glycolytic enzymes, vascular endothelial growth factor, and other genes whose protein products increase oxygen delivery or facilitate metabolic adaptation to hypoxia.	DR	PROSITE; PSS0112; PAS; 1.
CC	Plays an essential role in embryonic vascularization, tumor angiogenesis and pathophysiology of ischemic disease. Binds to core DNA sequence 5'-[AG]CGTG-3, within the hypoxia response element (HRE) of target gene promoters. Activation requires recruitment of transcriptional coactivators such as CREBPP and EP300. Activity is enhanced by interaction with both, NCOA1 or NCOA2. Interaction with redox regulatory protein APEX seems to activate CTAD and potentiates activation by NCOA1 and CREBPP (By similarity).	KW	Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein; Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
CC	-!- SUBUNIT: Efficient DNA binding requires heterodimerization of an alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of CREBPP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By similarity).	PT	Protein phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear translocation in response to hypoxia (By similarity).	DNA BIND	718 721
CC	-!- TISSUE SPECIFICITY: Expressed in the kidney, higher expression is seen in the renal medulla than in the cortex. Expressed also in the peri-venous zone of the liver.	DNA DOMAIN	718
CC	-!- DOMAIN: Contains two independent C-terminal transactivation domains, NTAD and CTAD, which function synergistically. Their transcriptional activity is repressed by an intervening inhibitory domain (ID) (By similarity).	DNA DOMAIN	717
CC	-!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-563 in the oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-563. The hydroxylated prolines promote interaction with VHL, initiating rapid ubiquitination and subsequent proteasomal degradation. Under hypoxia, proline hydroxylation is impaired and ubiquitination is attenuated, resulting in stabilization (By similarity).	DNA DOMAIN	720
CC	-!- PTM: In normoxia, is hydroxylated on Asn-802 by HIF1AN, thus abrogating interaction with CREBPP and EP300 and preventing transcriptional activation (By similarity).	DNA DOMAIN	720
CC	-!- PTM: S-nitrosylated. All free thiol groups are subjected to S-nitrosylation in vitro, however not all thiol groups seem to be nitrosylated in vivo (By similarity).	DNA DOMAIN	720
CC	-!- PTM: Acetylation of Lys-531 by ARD1 increases interaction with VHL and stimulates subsequent proteasomal degradation (By similarity).	DNA DOMAIN	720
CC	-!- PTM: Phosphorylation is required for DNA binding (By similarity).	DNA DOMAIN	720
CC	-!- SIMILARITY: Contains 1 basic helix-loop-helix (BHLH) domain.	DNA DOMAIN	720
CC	-!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.	DNA DOMAIN	720
CC	-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.	DNA DOMAIN	720
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	DR	Pfam; PF00010; HhH; 1.
CC	EMBL; AP057308; AAC24413.1; -.	DR	Pfam; PF00785; PAC; 1.
CC	HPSP; Q16665; 118C.	DR	Pfam; PF00989; PAS; 2.
CC	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
CC	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
CC	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
CC	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1; -.	DR	PROSITE; PSS0888; HhH; 1.
DR	EMBL; AP057308; AAC24413.1; -.	DR	PROSITE; PSS0112; PAS; 1.
DR	HPSP; Q16665; 118C.	DR	PROSITE; PSS0888; HhH; 1.
DR	TRANSFAC; T05461; -.	PRINTS	HYPOXIAIFIA.
DR	InterPro; IPR001092; HhH basic.	SMART	SM00353; HhH; 1.
DR	InterPro; IPR001321; Hypoxindia.	SMART	SM0086; PAC; 1.
DR	InterPro; IPR001610; PAC.	PROSITE	PSS0888; HhH; 1.
DR	InterPro; IPR000014; PAS.	DR	PROSITE; PSS0112; PAS; 1.
DR	EMBL; Y09507; CAA70701.1;		

RESULT 15

Q6EMI3 PRELIMINARY; PRT; 489 AA.

ID Q6EMI3; PRELIMINARY; PRT; 489 AA.

AC Q6EMI3; PRELIMINARY; PRT; 489 AA.

DT 25-OCT-2004 (TREMBLrel. 28, Created)

DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)

DE Hypoxia-inducible factor 1 alpha (Fragment).

OS Xenopus laevis (African clawed frog).

OC Amphibia; Batrachia; Anura; Mesobatrachia; Craniata; Vertebrata; Buteleostomi; Xenopodinae; Xenopus.

OC NCBI_TaxID=8355;

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=liver;

RX PubMed=15162502; DOI=10.1002/dvdy.20049;

RA Sipe C.W., Gruber B.J., Saha M.S.;

RT "Short upstream region drives dynamic expression of hypoxia-inducible factor 1alpha during Xenopus development.";

RL Dev. Dyn. 230:229-238 (2004).

CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

DR EMBL; AV189821; AA072733; 1; -.

DR GO; GO:0005634; C-nucleus; IEA.

DR GO; GO:0004871; F-signaling transducer activity; IEA.

DR GO; GO:003700; F-transcription factor activity; IEA.

DR GO; GO:0005355; P-regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0007165; P-signaling transduction; IEA.

DR InterPro; IPR001032; HLH basic.

DR InterPro; IPR001321; HypoxidinRia.

DR InterPro; IPR001067; Nuc_transllocat.

DR InterPro; IPR001610; PAC.

DR InterPro; IPR000014; PAS.

DR Pfam; PF00010; HLH; 1.

DR Pfam; PF000785; PAC; 1.

DR Pfam; PF00989; PAS; 2.

DR PRINTS; PR01080; HYPOKAIFI.

DR SMART; SM0053; HLH; 1.

DR SMART; SM00086; PAC; 1.

DR SMART; SM00091; PAS; 2.

DR PROSITE; PS50888; HLH; 1.

DR PROSITE; PS50112; PAS; 2.

FT NON_TER 1

FT NON_TER 489 AA; 55613 MW; 3981AC3EA6AF766 CRC64;

SQ SEQUENCE 489 AA; 55613 MW; 3981AC3EA6AF766 CRC64;

Query Match 30.3%; Score 495; DB 2; Length 489;

Best Local Similarity 49.6%; Pred. No. 1.2e-32; Mismatches 71; Indels 18; Gaps 6;

Matches 114; Conservative 27; Mismatches 71; Indels 18; Gaps 6;

QY 13 ERKEKSRDARSRSRQETEVLYKQAHIPPARCYSAHLDKASMRLLTISYRMLRLCA 72

Db 1 ERKEKSRDARSRSRQETEVLYKQAHIPPARCYSAHLDKASMRLLTISYRMLRLCA 60

QY 73 GKGKGRTGRATGRGLPSPGGGRHGRGGRHGRGGLPVRCQQAPGPOSVDLGCSSLTHNPTGC- 131

Db 61 GDLGEGTD--LDKLNCF--YIKALEGFPVLVLTBEG---DMYLSEVNKCML 107

QY 132 TNFSFELIGHISIFPFRPCDQEELQDALIPRPNLSKKLLEAPTERHFSLRMKSTLTSRGR 191

Db 108 TQF--ELTGHSVFDFTHPCDHEELREMLPFRNGPAKKGEQITERSFFLRMKCTVTSRGR 165

QY 192 TLNQKAATWKLHGSCHMAYKPPAQTSFAGSPRSEPPILQCLVILCEAIP 241

Db 166 TUNIKSATWKVHLCTIGHMRYVVDANNOKICG--YKKPPKCMVWICPIP 213

Search completed: June 15, 2005, 16:00:09

Job time : 176 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2005, 16:00:19 ; Search time 157 Seconds

(Without alignments)

749.578 Million cell updates/sec

Title: US-09-896-791B-3
Perfect score: 1636
Sequence: 1 MAIGLQRVRSNTLRLKEKSR.....TESSLUPSWVLMALNRRKNCPG 307
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters:

1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cn2_6/ptodata/1/pubpaa/us07_pubcomb.pep: *
2: /cn2_6/ptodata/1/pubpaa/pctv_new_pub.pep: *
3: /cn2_6/ptodata/1/pubpaa/us06_pubcomb.pep: *
4: /cn2_6/ptodata/1/pubpaa/us07_new_pub.pep: *
5: /cn2_6/ptodata/1/pubpaa/pctv_pubcomb.pep: *
6: /cn2_6/ptodata/1/pubpaa/us08_new_pub.pep: *
7: /cn2_6/ptodata/1/pubpaa/us09_pubcomb.pep: *
8: /cn2_6/ptodata/1/pubpaa/us09_pubcomb.pep: *
9: /cn2_6/ptodata/1/pubpaa/us09_pubcomb.pep: *
10: /cn2_6/ptodata/1/pubpaa/us09_pubcomb.pep: *
11: /cn2_6/ptodata/1/pubpaa/us10_pubcomb.pep: *
12: /cn2_6/ptodata/1/pubpaa/us10_pubcomb.pep: *
13: /cn2_6/ptodata/1/pubpaa/us10_pubcomb.pep: *
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15: /cn2_6/ptodata/1/pubpaa/us10d_pubcomb.pep: *
16: /cn2_6/ptodata/1/pubpaa/us10e_pubcomb.pep: *
17: /cn2_6/ptodata/1/pubpaa/us10_new_pub.pep: *
18: /cn2_6/ptodata/1/pubpaa/us11_pubcomb.pep: *
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20: /cn2_6/ptodata/1/pubpaa/us60_pubcomb.pep: *
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22: /cn2_6/ptodata/1/pubpaa/us60_pubcomb.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1636	100.0	307	9 US-09-896-791B-3	Sequence 3, Appli
2	1278	78.1	324	15 US-10-307-928A-20	Sequence 20, Appli
3	795	48.6	705	14 US-15-154-386-2	Sequence 2, Appli
4	498	30.4	827	10 US-09-910-039-149	Sequence 19, Appli
5	498	30.4	827	14 US-10-247-671-137	Sequence 17, Appli
6	495	30.3	623	10 US-09-867-388-2	Sequence 2, Appli
7	495	30.3	735	16 US-10-032-561-2	Sequence 2, Appli
8	495	30.3	826	9 US-09-922-958-4	Sequence 4, Appli
9	495	30.3	826	9 US-09-833-79-235	Sequence 23, Appli
10	495	30.3	826	9 US-09-736-457-330	Sequence 330, Appli
11	495	30.3	826	9 US-09-902-941-330	Sequence 330, Appli

RESULT 1
US-09-896-791B-3
; Sequence 3, Application US/0996791B
; Patent No. US20020165140A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Bertilsson, Gran
; APPLICANT: Poellinger, Lorenz
; TITLE OF INVENTION: SCREENING METHODS
; FILE REFERENCE: 13-25-04-001
; CURRENT APPLICATION NUMBER: US/09/896,791B
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/217,570
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: SE 0002551-0
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-896-791B-3

Query Match 100.0%; Score 1636; DB 9; Length 307;
Best Local Similarity 100.0%; Pred. No. 6; 3e-146; Length 307;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIGLQRVRSNTLRLKEKSRDAARSRSQETEVLYQALTLPPARGVSAHLKASIMLT 60
Dy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1 MAIGLQRVRSNTLRLKEKSRDAARSRSQETEVLYQALTLPPARGVSAHLKASIMLT 60

QY 61 ISYARMHRLCAAGGKRGKGRGATGRGLPPEGGGPRGHGTHRGRHGLPVGKQQAPCQPSVILC 120
Dy ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 61 ISVLRMHRLCAAGGKGRATGRGLLPEGPGFRFRGTHRGRHGLPVGKQQAEGPQSYDLC 120
 QY 121 SSLJHNPPGTGNTSLEIIGHS.FDFIHCQDQEFLQDALTPRPNLSKKLEAPTERHSL 180
 Db 121 SSSLJHNPPGTGNTSLEIIGHS.FDFIHCQDQEFLQDALTPRPNLSKKLEAPTERHSL 180
 QY 181 RMKSTLTSRGRTLNKAATWKVLUHCSGHMRAKYKPAQTSPGSPRSEPPLOCLVILCEAI 240
 Db 181 RMKSTLTSRGRTLNKAATWKVLUHCSGHMRAKYKPAQTSPGSPRSEPPLOCLVILCEAI 240
 QY 241 PQLPHDGATLGLPOEKTISTLTPLWALKLIVKRPVQVLOGKGPESLSSWVIAL 300
 Db 241 PQLPHDGATLGLPOEKTISTLTPLWALKLIVKRPVQVLOGKGPESLSSWVIAL 300
 QY 301 NRKNCPG 307
 Db 301 NRKNCPG 307

RESULT 2
 US-10-307-928A-20
 ; Sequence 20, Application US/10307928A
 ; Publication No. US20030229016A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook, John P.
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia (Sasha)
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Li, Li
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Reiger, Daniel K.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Vernet, Corinne A.M.
 ; APPLICANT: Voss, Edward Z.
 ; APPLICANT: Zheng, Mei
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
 ; TITLE OF INVENTION: THE SAME
 ; FILE REFERENCE: 24102-502D
 ; CURRENT APPLICATION NUMBER: US/10/307,928A
 ; CURRENT FILING DATE: 2002-12-02
 ; PRIOR APPLICATION NUMBER: 6/0/341,477
 ; PRIOR FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: 6/0/341,540
 ; PRIOR FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: 6/0/342,592
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: 6/0/344,903
 ; PRIOR FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: 6/0/373,288
 ; PRIOR FILING DATE: 2002-04-17
 ; PRIOR APPLICATION NUMBER: 6/0/380,981
 ; PRIOR FILING DATE: 2002-05-15
 ; PRIOR APPLICATION NUMBER: 6/0/381,495
 ; PRIOR FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 6/0/383,744
 ; PRIOR FILING DATE: 2002-05-28
 ; PRIOR APPLICATION NUMBER: 6/0/384,024
 ; PRIOR FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: 6/0/401,788
 ; PRIOR FILING DATE: 2002-08-07
 ; Remaining Prior Application data removed - See File wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: CuraseqList version 0.1
 ; SEQ ID NO 20
 ; LENGTH: 324
 ; TYPE: PRT

Db ; ORGANISM: Homo sapiens
 ; US-10-307-928A-20
 ; Query Match 78.1%; Score 1278; DB 15; Length 324;
 ; Best Local Similarity 79.9%; Pred. No. 4 6e-12;
 ; Matches 250; Conservative 14; Mismatches 41; Indels 8; Gaps 3;
 QY 1 MALGQVRNSNTELKEKSQDARSRSQETEVLYQAHTLPPARGVSAHLDKASIMRLT 60
 Db 1 MALGQVRNSNTELKEKSQDARSRSQETEVLYQAHTLPPARGVSAHLDKASIMRLT 60
 QY 61 ISVLRMHRLCAAGGKGRATGRGLLPEGPGFRFRGTHRGRHGLPVGKQQAEGPQSYDLC 120
 Db 61 ISVLRMHRLCAAGGKGRATGRGLLPEGPGFRFRGTHRGRHGLPVGKQQAEGPQSYDLC 120
 QY 121 SSSLJHNPPGTGNTSLEIIGHS.FDFIHCQDQEFLQDALTPRPNLSKKLEAPTERHSL 180
 Db 121 SSSLJHNPPGTGNTSLEIIGHS.FDFIHCQDQEFLQDALTPRPNLSKKLEAPTERHSL 180
 QY 181 RMKSTLTSRGRTLNKAATWKVLUHCSGHMRAKYKPAQTSPGSPRSEPPLOCLVILCEAI 240
 Db 181 RMKSTLTSRGRTLNKAATWKVLUHCSGHMRAKYKPAQTSPGSPRSEPPLOCLVILCEAI 240
 QY 241 PQLPHDGATLGLPOEKTISTLTPLWALKLIVKRPVQVLOGKGPESLSSWVIAL 300
 Db 241 PQLPHDGATLGLPOEKTISTLTPLWALKLIVKRPVQVLOGKGPESLSSWVIAL 300
 QY 301 NRKNCPG 307
 Db 301 NRKNCPG 307

RESULT 3
 US-10-154-386-2
 ; Sequence 2, Application US/10154386
 ; Publication No. US2003026793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guy, Louis Georges
 ; APPLICANT: Angiogene Inc.
 ; TITLE OF INVENTION: HIFXOXA INDUCING FACTORS AND USES THEREOF FOR INDUCING ANGIOGENESIS
 ; FILE REFERENCE: 5600-81
 ; CURRENT APPLICATION NUMBER: US/10/154,386
 ; CURRENT FILING DATE: 2002-05-23
 ; PRIOR APPLICATION NUMBER: US 60/292,630
 ; PRIOR FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 60/354529
 ; PRIOR FILING DATE: 2002-02-08
 ; NUMBER OF SEQ ID NOS: 13
 ; SEQ ID NO 2
 ; LENGTH: 705
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-154-386-2
 ; Query Match 48.6%; Score 795; DB 14; Length 705;
 ; Best Local Similarity 67.6%; Pred. No. 5. 6e-66;
 ; Matches 171; Conservative 11; Mismatches 29; Indels 42; Gaps 5;
 QY 9 RSTELERKEKSQDARSRSQETEVLYQAHTLPPARGVSAHLDKASIMRLTISYMR 68
 Db 9 RSTELERKEKSQDARSRSQETEVLYQAHTLPPARGVSAHLDKASIMRLTISYMR 68
 QY 3 RSTELERKEKSQDARSRSQETEVLYQAHTLPPARGVSAHLDKASIMRLTISYMR 62
 QY 69 LCAAGGKGRATGRGLLPEGPGFRFRGTHRGRHGLPVGKQO-----QAPGQOSV 117
 Db 69 LCAAGGKGRATGRGLLPEGPGFRFRGTHRGRHGLPVGKQO-----QAPGQOSV 117
 QY 63 LCAAGGKGRATGRGLLPEGPGFRFRGTHRGRHGLPVGKQO-----QAPGQOSV 102
 Db 118 DLQSSSLJHNPPGTGNTS-LEIIGHS.FDFIHCQDQEFLQDALTPRPNLSKKLEAPTERHSL 176
 QY 103 -----LSENVSKHGLSSELEIIGHS.FDFIHCQDQEFLQDALTPRPNLSKKLEAPTER 156
 QY 177 HFSLRMKSTLTSRGRTLNKAATWKVLUHCSGHMRAKYKPAQTSPGSPRSEPPLOCLVIL 236

RESULT 4
US-09-919-039-149
; Sequence 149, Application US/03919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CD1
; US-09-919-039-149

Query Match 30.4%; Score 498; DB 10; Length 827;
Best Local Similarity 46.2%; Pred. No. 8e-38; Mismatches 60; Indels 48; Gaps 6;
Matches 115; Conservative 26; Mismatches 60; Indels 48; Gaps 6;

QY 9 RSNTELKEKRSRDAARSRSRSQETEVLYQLAHTLPARGVSAHDKASIMRLTISYLRMR 68
Db 13 RISSERKEKRSRDAARSRSRSKESEVYELAHOLPLPHNVSSHLDKASVWRLTISYLRK 72
QY 69 LCAAGGKRGRATGRLLPQPGGFRHGRHGRGLPVGKQQA----- PGPQSVD 118
Db 73 LDAG----- DLDIDDMKAQMCYTLKALDGFWML 104
QY 119 LCSSSLIH---NPTPG-TNFSLELIGHSIFPHTHEDQEEQDALTPRPNLSPRSKKEA 172
Db 105 TDDCDMIXYSDNTNKYMDITP-ELTGSVDFTHPCOHEEMRLTHNGLKVKGQ 162
QY 173 PTERHPSLKMSTTSRGRTLNKAATWKVLUHSGHMRAYKPPAQTSAGSPRSBPPQC 232
Db 163 NTQSFPLRJKCUTSRRTMNKSAATWKVLUHCTGHTHVTIDTNSNQPCG--YKPPWTC 220
QY 233 LVLICEAIP 241
Db 221 LVLICEAIP 229

RESULT 5
US-10-247-671-137
; Sequence 137, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: MIKITA, Thomas
; APPLICANT: Schiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program

Query Match 30.3%; Score 495; DB 10; Length 623;
Best Local Similarity 46.2%; Pred. No. 1-1e-37; Mismatches 59; Indels 48; Gaps 6;
Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

QY 11 NTELKEKRSRDAARSRSRSQETEVLYQLAHTLPARGVSAHDKASIMRLTISYLRUC 70
Db 14 SSERKEKRSRDAARSRSRSKESEVYELAHOLPLPHNVSSHLDKASVWRLTISYLRU 73
QY 71 AAGGKRGRATGRLLPQPGGFRHGRHGRGLPVGKQQA----- PGPQSVDLC 120
Db 74 DAG----- DLDIDDMKAQMCYTLKALDGFWML 105
QY 121 SSSLIH---NPTPG-TNFSLELIGHSIFPHTHEDQEEQDALTPRPNLSPRSKKEA 174
Db 106 DGDMDIVYSDNTNKYMDITP-ELTGSVDFTHPCOHEEMRLTHNGLKVKGQNT 163
QY 175 ERHPSLKMSTTSRGRTLNKAATWKVLUHSGHMRAYKPPAQTSAGSPRSBPPQCIV 234
Db 164 QSFPLRJKCUTSRRTMNKSAATWKVLUHCTGHTHVTIDTNSNQPCG--YKPPWTCIV 221

RESULT 7

US-10-032-361-2

Sequence 2, Application US/10032361

Publication No. US20040214777A1

GENERAL INFORMATION:

APPLICANT: McGrath, Kevin

TITLE OF INVENTION: Peptide Activators of VEGF

FILE REFERENCE: 1443_025051

CURRENT APPLICATION NUMBER: US10/032,361

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 735

TYPE: PRT

ORGANISM: Homo sapiens

US-10-032-361-2

Query Match 30.3%; Score 495; DB 16; Length 735;

Best Local Similarity 46.2%; Pred. No. 1.3e-37;

Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

Qy 11 NTELREKRSRDAARSRSRQETEVLYQLAHTIPFARGVS AHLDKASIMRLTISYLRMRLC 70

Db 14 SSERREKRSRDAARSRSRQETEVLYQLAHTIPFARGVS AHLDKASIMRLTISYLRMRLC 70

Qy 71 AAGGKRGRATRQLLPQPGGGRRHGRGHLGVPKCQQA----- PGPSV DLC 120

Db 74 DAG----- DLDI DDMKQMCYFLKALDG FVWV LTD 105

Qy 121 SSSLIH----NPTPG-TNFSLELGHISI EFTI PCDQEELQDALTPRPNISKKKLEAPT 174

Db 106 DGDMDTISDNVNKYMGTQF--ELTHGSVFDTHPCDHEEMRMLTHRNGLVKGKBEQNT 163

Qy 175 ERHFSRMRKSLTSRGRTRNLKAATKVKLQHGSGHMRAYKPAQTS PAGSPSPBPPQCLV 234

Db 164 QRSFELRMKCTLTSRGRTRNLKAATKVKLQHGSGHMRAYKPAQTS PAGSPSPBPPQCLV 221

Qy 235 LICEAIP 241

Db 222 LICEPIP 228

RESULT 8

US-09-922-958-4

Sequence 4, Application US/09922958

PATENT NO. US20020048794A1

GENERAL INFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Wang, Tongtong

APPLICANT: Secrist, Heather

APPLICANT: Mohanath, Raodoh

APPLICANT: Indrias, Carol Y.

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121_512

CURRENT APPLICATION NUMBER: US/09/833,790

CURRENT FILING DATE: 2001-04-11

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 235

LENGTH: 826

TYPE: PRT

ORGANISM: Homo sapiens

US-09-833-790-235

Query Match 30.3%; Score 495; DB 9; Length 826;

Best Local Similarity 46.2%; Pred. No. 1.5e-37;

Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

Qy 11 NTELREKRSRDAARSRSRQETEVLYQLAHTIPFARGVS AHLDKASIMRLTISYLRMRLC 70

Db 14 SSERREKRSRDAARSRSRQETEVLYQLAHTIPFARGVS AHLDKASIMRLTISYLRMRLC 70

Qy 71 AAGGKRGRATRQLLPQPGGGRRHGRGHLGVPKCQQA----- PGPSV DLC 120

Db 74 DAG----- DLDI DDMKQMCYFLKALDG FVWV LTD 105

Qy 121 SSSLIH----NPTPG-TNFSLELGHISI EFTI PCDQEELQDALTPRPNISKKKLEAPT 174

Db 106 DGDMDTISDNVNKYMGTQF--ELTHGSVFDTHPCDHEEMRMLTHRNGLVKGKBEQNT 163

Qy 175 ERHFSRMRKSLTSRGRTRNLKAATKVKLQHGSGHMRAYKPAQTS PAGSPSPBPPQCLV 234

Db 164 QRSFELRMKCTLTSRGRTRNLKAATKVKLQHGSGHMRAYKPAQTS PAGSPSPBPPQCLV 221

Qy 235 LICEAIP 241

Db 222 LICEPIP 228

Sequence 330, Application US/09735457
 Patent No. US20020168637A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Tongtong
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Lodes, Michael A.
 APPLICANT: Fang, Aijun
 APPLICANT: Vedula, Tom
 APPLICANT: Carter, Darrick
 APPLICANT: Retter, Marc
 APPLICANT: Mannion, Jane
 APPLICANT: Fan, Liqun
 APPLICANT: Wang, Aijun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121-478C15
 CURRENT APPLICATION NUMBER: US/09/736,457
 CURRENT FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 1864
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 330
 LENGTH: 826
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-736-457-330
 Query Match 30.3%; Score 495; DB 9; Length 826;
 Best Local Similarity 46.2%; Pred. No. 1.5e-37;
 Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;
 Qy 11 NTELKEKRSRDAARSRSRQETEVLYQLAHTLPARGVS AHLKASIMRLTISYLMRHLIC 70
 Db 14 SSERRKEKRSRDAARSRSRQETEVLYQLAHTLPARGVS AHLKASIMRLTISYLMRHLIC 70
 Qy 71 AAGGKRGRATGRLLPPEGPGFRHGRGRHGLPVGKQQA-----PGPOSVDLC 120
 Db 74 DAG-----DLDIEDDMQACQMCYFLKALDGFMVLTD 105
 Qy 121 SSSLIH----NPTEG-TNFSLEIGHSTFDIHPQDQEQLDALTPRPNLSKKEAAPT 174
 Db 106 DGDMDYISDNWKYNGLTOF--ELTHGSVFDFTHPCDHEEMRLTHNGLVIKKGKQEQT 163
 Qy 175 ERHFSIRMKSLTTSRGRTLNKAATWKVHLHSGHRAKPAQTSPAGSSRSEPIQCLV 234
 Db 164 QRSFPLRMKCTLTTSRGRTMNKISATWKVHLHSGHRAKPAQTSPAGSSRSEPIQCLV 221
 Qy 176 ERHFSIRMKSLTTSRGRTLNKAATWKVHLHSGHRAKPAQTSPAGSSRSEPIQCLV 234
 Db 164 QRSFPLRMKCTLTTSRGRTMNKISATWKVHLHSGHRAKPAQTSPAGSSRSEPIQCLV 221
 Qy 235 LICEAIP 241
 Db 222 LICEAIP 228
 RESULT 12
 US-09-849-626-330
 Sequence 330, Application US/09849626
 Publication No. US20020197669A1
 GENERAL INFORMATION:
 APPLICANT: Bangur, Chaitanya
 APPLICANT: Fang, Aijun
 APPLICANT: Wang, Aijun
 APPLICANT: Wang, Tongtong
 APPLICANT: Switzer, Anne
 APPLICANT: McNeill, Patricia
 APPLICANT: Clapper, Jonathan
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121-478C15
 CURRENT APPLICATION NUMBER: US/09/849,626
 CURRENT FILING DATE: 2001-05-03
 NUMBER OF SEQ ID NOS: 1926
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 330
 LENGTH: 826
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-849-626-330
 Query Match 30.3%; Score 495; DB 9; Length 826;
 Best Local Similarity 46.2%; Pred. No. 1.5e-37;
 Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;
 Qy 11 NTELKEKRSRDAARSRSRQETEVLYQLAHTLPARGVS AHLKASIMRLTISYLMRHLIC 70
 Db 14 SSERRKEKRSRDAARSRSRQETEVLYQLAHTLPARGVS AHLKASIMRLTISYLMRHLIC 70
 Qy 71 AAGGKRGRATGRLLPPEGPGFRHGRGRHGLPVGKQQA-----PGPOSVDLC 120
 Db 74 DAG-----DLDIEDDMQACQMCYFLKALDGFMVLTD 105
 Qy 121 SSSLIH----NPTEG-TNFSLEIGHSTFDIHPQDQEQLDALTPRPNLSKKEAAPT 174
 Db 106 DGDMDYISDNWKYNGLTOF--ELTHGSVFDFTHPCDHEEMRLTHNGLVIKKGKQEQT 163

Thu Jun 16 13:05:40 2005

usb-09-896-791b-3.rapb

Page 7

Qy 235 LICEPIP 241.
| | | | |
Db 222 LICEPIP 228

Search completed: June 15, 2005, 16:13:41
Job time : 159 secs

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Om protein - protein search, using sw model

Run on: June 15, 2005, 15:50:48 ; Search time 42 Seconds

Sequence: 1 MALGIQVRVRSNTELRKKEKR.....TESSLPSWVLMALNLRKNCPG 307 (without alignments) 545.649 Million cell updates/sec

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0‡ Maximum Match 100‡

Listing first 45 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/ptodata/1/iaa/6A/COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B/COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCUS/COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backflesl.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

‡

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	498	30.4	827	4	US-09-919-039-149		Sequence 149, App
2	495	30.3	245	4	US-09-438-833-3		Sequence 3, Appli
3	495	30.3	330	4	US-09-438-833-4		Sequence 4, Appli
4	495	30.3	623	4	US-09-438-833-5		Sequence 2, Appli
5	495	30.3	652	4	US-09-438-833-5		Sequence 5, Appli
6	495	30.3	813	4	US-09-438-833-12		Sequence 12, Appli
7	495	30.3	825	4	US-09-438-833-12		Sequence 6, Appli
8	495	30.3	826	2	US-09-480-473B-2		Sequence 2, Appli
9	495	30.3	826	3	US-09-919-213-2		Sequence 2, Appli
10	495	30.3	825	3	US-09-143-547-2		Sequence 2, Appli
11	495	30.3	826	3	US-09-235-217-2		Sequence 2, Appli
12	495	30.3	826	3	US-09-380-662-23		Sequence 23, Appli
13	495	30.3	825	4	US-09-438-833-1		Sequence 1, Appli
14	495	30.3	826	4	US-09-702-705-330		Sequence 2, Appli
15	495	30.3	826	4	US-09-736-457-330		Sequence 330, App
16	495	30.3	825	4	US-09-383-581-2		Sequence 2, Appli
17	495	30.3	826	4	US-09-611-124B-330		Sequence 330, App
18	495	30.3	826	4	US-09-671-325-330		Sequence 330, App
19	495	30.3	825	4	US-09-589-184-330		Sequence 330, App
20	495	30.3	826	4	US-09-658-824-330		Sequence 330, App
21	495	30.3	826	4	US-09-959-873B-18		Sequence 18, Appli
22	495	30.3	825	4	US-09-949-016-6089		Sequence 6089, Appli
23	495	30.3	826	4	US-09-967-388-4		Sequence 4, Appli
24	495	30.3	826	5	PCT-US96-10251-2		Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-09-919-039-149
Sequence 149, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: KASPER, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-05-09
; PRIORITY APPLICATION NUMBER: 60/222,113
; PRIORITY FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1250434CD1
; US-09-919-039-149
Query Match 30.4%; Score 498; DB 4; Length 827;
Best Local Similarity 46.2%; Pred. No. 1.4e-45;
Matches 115; Conservative 26; Mismatches 60; Indels 48; Gaps 6;
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Sequence 3, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438, 833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 245
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Subdomain
OTHER INFORMATION: 1-245 of human HIF-1 alpha
US-09-438-833-3

Query Match
Best Local Similarity 30.3%; Score 495; DB 4; Length 245;
Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;
Qy 11 NTELKEKRSRDAARSRSQETEVLYQLAHTIPFARGVSAHLDKASIMRLTISYLRMHLRC 70
Db 14 SSERKEKRSRDAARSRSQETEVLYQLAHTIPFARGVSAHLDKASIMRLTISYLRMHLRC 70
Qy 71 AAGGKRGRATGRILLPGPGFPRHGTRGRHGLPGVKGQQA-----PGPQSVDLC 120
Db 74 DAG-----DLDIETDMKQMNCFYKALDGVFMVILTD 105
Qy 121 SSSLH-----NPTPG-TNFSLELTGHISIDFDPICDQEELQDALTPRENTSKKLEAPT 174
Db 106 DGDMDTISDNVNKYMGLTOF-ELTGHSVFDFTHPCDHEBEMRLTNGLVKGKEONT 163
Qy 175 ERHFSLARKSTLTSRGRTLANKAATWKVLUHCSHMRAYKPAQTSPAGSPSPSEPPQCLV 234
Db 164 QSFPLRMKCTLSRGRTMNIKSATWKVLUHCTGHIVDNTSNQPGCG--YKKPMPMCLV 221
Qy 235 LICEAIP 241
Db 222 LICEPIP 228

RESULT 3
US-09-438-833-4
; Sequence 4, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438, 833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 623
TYPE: PRT
ORGANISM: HUMAN
US-09-967-388-2

Query Match
Best Local Similarity 30.3%; Score 495; DB 4; Length 623;
Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;
Qy 11 NTELKEKRSRDAARSRSQETEVLYQLAHTIPFARGVSAHLDKASIMRLTISYLRMHLRC 70
Db 14 SSERKEKRSRDAARSRSQETEVLYQLAHTIPFARGVSAHLDKASIMRLTISYLRMHLRC 70
Qy 71 AAGGKRGRATGRILLPGPGFPRHGTRGRHGLPGVKGQQA-----PGPQSVDLC 120
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Qy 121 SSSLH-----NPTPG-TNFSLELTGHISIDFDPICDQEELQDALTPRPNISKKLEAPT 174
Db 106 DGDMDTISDNVNKYMGLTOF-ELTGHSVFDFTHPCDHEBEMRLTNGLVKGKEONT 163
Qy 175 ERHFSLARKSTLTSRGRTLANKAATWKVLUHCSHMRAYKPAQTSPAGSPSPSEPPQCLV 234
Db 164 QSFPLRMKCTLSRGRTMNIKSATWKVLUHCTGHIVDNTSNQPGCG--YKKPMPMCLV 221
Qy 235 LICEAIP 241
Db 222 LICEPIP 228

RESULT 4
US-09-967-388-2
; Sequence 2, Application US/09967388
; Patent No. 6838430
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. ARBIT
; TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
; TITLE OF INVENTION: WOUND HEALING
; FILE REFERENCE: UC077-001A
; CURRENT APPLICATION NUMBER: US/09/967, 388
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 623
; TYPE: PRT
; ORGANISM: HUMAN
US-09-967-388-2

Query Match
Best Local Similarity 30.3%; Score 495; DB 4; Length 623;
Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;
Qy 11 NTELKEKRSRDAARSRSQETEVLYQLAHTIPFARGVSAHLDKASIMRLTISYLRMHLRC 70
Db 14 SSERKEKRSRDAARSRSQETEVLYQLAHTIPFARGVSAHLDKASIMRLTISYLRMHLRC 70
Qy 71 AAGGKRGRATGRILLPGPGFPRHGTRGRHGLPGVKGQQA-----PGPQSVDLC 120
Db 74 DAG-----DLDIETDMKQMNCFYKALDGVFMVILTD 105
Qy 121 SSSLH-----NPTPG-TNFSLELTGHISIDFDPICDQEELQDALTPRPNISKKLEAPT 174
Db 106 DGDMDTISDNVNKYMGLTOF-ELTGHSVFDFTHPCDHEBEMRLTNGLVKGKEONT 163
Qy 175 ERHFSLARKSTLTSRGRTLANKAATWKVLUHCSHMRAYKPAQTSPAGSPSPSEPPQCLV 234
Db 164 QSFPLRMKCTLSRGRTMNIKSATWKVLUHCTGHIVDNTSNQPGCG--YKKPMPMCLV 221
Qy 235 LICEAIP 241
Db 222 LICEPIP 228

RESULT 5
US-09-438-833-5
; Sequence 5, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438, 833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
Qy 11 NTELKEKRSRDAARSRSQETEVLYQLAHTIPFARGVSAHLDKASIMRLTISYLRMHLRC 70
Db 14 SSERKEKRSRDAARSRSQETEVLYQLAHTIPFARGVSAHLDKASIMRLTISYLRMHLRC 70
Qy 175 ERHFSLARKSTLTSRGRTLANKAATWKVLUHCSHMRAYKPAQTSPAGSPSPSEPPQCLV 234
Db 164 QSFPLRMKCTLSRGRTMNIKSATWKVLUHCTGHIVDNTSNQPGCG--YKKPMPMCLV 221
Qy 235 LICEAIP 241
Db 222 LICEPIP 228

```

;

SEQ ID NO 5 LENGTH: 652

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Subdomain US-09-438-833-5,

Query Match 30.3%; Score 495; DB 4; Length 652; Best Local Similarity 46.2%; Pred. No. 2.1e-45; Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

QY 11 NTELKEKERSDAARSRRSRSQETEVLYQALHTLPPARGVSAHLDKASIMRLTISYLRMHLIC 70

Db 14 SSERKEKERSDAARSRRSRSKESEVYELAHOLPLPHNVSILDKASIMRLTISYLRVRLIC 73

QY 71 AAGGKRGRATGRLLPPEGPGFRHGRHGLPGVKCQA-----PSQPSVDC 120

Db 74 DAG-----DLDIEDDKAQMCYFLKALDGFMVLTD 105

Db 121 SSSLIH---NPTPG-TNPSLEIGHSTDFTHPCDQEELQALTPTPNLSKCKLAPT 174

QY 106 DGDMMIYISDNVNKYMLQT-----ELTGHSVFDTHPCDHEMRLTHNGLVKGKQNT 163

Db 106 DGDMMIYISDNVNKYMLQT-----ELTGHSVFDTHPCDHEMRLTHNGLVKGKQNT 163

QY 106 DGDMMIYISDNVNKYMLQT-----ELTGHSVFDTHPCDHEMRLTHNGLVKGKQNT 163

Db 175 ERHFSLRMKSTLTSQRTNLKAATWKVLUHCSGMRAYKPPAOTSPAGSPRSEPPLOCV 234

QY 164 ORSFPLRMKCTLSRGRTRNNIKSAATWKVLCTGHIHVYDTSNQPQCG--YKKPMTCLV 221

Db 235 LICEAIP 241

QY 222 LICEPIP 228

RESULT 6

US-09-438-833-12

Sequence 12, Application US/09438833

Patent No. 6,436,654

GENERAL INFORMATION:

APPLICANT: Pharmacia & Upjohn

TITLE OF INVENTION: Protein variants

FILE REFERENCE: 1848

CURRENT APPLICATION NUMBER: US/09/438, 833

CURRENT FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 15

SEQUENCE ID NO: 12

SEQ ID NO: 12 LENGTH: 813

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Subdomain US-09-438-833-12

Query Match 30.3%; Score 495; DB 4; Length 813; Best Local Similarity 46.2%; Pred. No. 2.9e-45; Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

QY 11 NTELKEKERSDAARSRRSRSQETEVLYQALHTLPPARGVSAHLDKASIMRLTISYLRMHLIC 70

Db 14 SSERKEKERSDAARSRRSRSKESEVYELAHOLPLPHNVSILDKASIMRLTISYLRVRLIC 73

QY 71 AAGGKRGRATGRLLPPEGPGFRHGRHGLPGVKCQA-----PSQPSVDC 120

Db 74 DAG-----DLDIEDDKAQMCYFLKALDGFMVLTD 105

Db 121 SSSLIH---NPTPG-TNPSLEIGHSTDFTHPCDQEELQALTPTPNLSKCKLAPT 174

QY 106 DGDMMIYISDNVNKYMLQT-----ELTGHSVFDTHPCDHEMRLTHNGLVKGKQNT 163

Db 175 ERHFSLRMKSTLTSQRTNLKAATWKVLUHCSGMRAYKPPAOTSPAGSPRSEPPLOCV 234

QY 164 ORSFPLRMKCTLSRGRTRNNIKSAATWKVLCTGHIHVYDTSNQPQCG--YKKPMTCLV 221

Db 235 LICEAIP 241

Db 222 LICEPIP 228

RESULT 7

US-08-785-241-6

Sequence 6, Application US/08785241

Patient No. 5,695,963

GENERAL INFORMATION:

APPLICANT: McKnight, Steven L.

APPLICANT: Russell, David W.

TITLE OF INVENTION: Endothelial PAS Domain Protein

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/785, 241

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UTSD:1229

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 826 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-785-241-6

Query Match 30.3%; Score 495; DB 1; Length 826; Best Local Similarity 46.2%; Pred. No. 3e-45; Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

QY 11 NTELKEKERSDAARSRRSRSQETEVLYQALHTLPPARGVSAHLDKASIMRLTISYLRMHLIC 70

Db 14 SSERKEKERSDAARSRRSRSKESEVYELAHOLPLPHNVSILDKASIMRLTISYLRVRLIC 73

QY 71 AAGGKRGRATGRLLPPEGPGFRHGRHGLPGVKCQA-----PSQPSVDC 120

Db 74 DAG-----DLDIEDDKAQMCYFLKALDGFMVLTD 105

Db 121 SSSLIH---NPTPG-TNPSLEIGHSTDFTHPCDQEELQALTPTPNLSKCKLAPT 174

QY 106 DGDMMIYISDNVNKYMLQT-----ELTGHSVFDTHPCDHEMRLTHNGLVKGKQNT 163

Db 175 ERHFSLRMKSTLTSQRTNLKAATWKVLUHCSGMRAYKPPAOTSPAGSPRSEPPLOCV 234

QY 164 ORSFPLRMKCTLSRGRTRNNIKSAATWKVLCTGHIHVYDTSNQPQCG--YKKPMTCLV 221

Db 235 LICEAIP 241

Db 222 LICEPIP 228

RESULT 8
 US-08-480-473B-2
 ; Sequence 2, Application US/08480473B
 ; Patent No. 5882914
 ; GENERAL INFORMATION:
 ; APPLICANT: Semenza, Gregg L.
 ; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,473B
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5059
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 826 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; US-08-480-473B-2

Query Match 30.3%; Score 495; DB 2; Length 826;
 Best Local Similarity 45.2%; Pred. No. 3-e-45; Mismatches 59; Indels 48; Gaps 6;
 Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

Qy 11 NTELKEKERSDAARSRSRQETEVYQALHTLPFARGVSAHLKASIMULTISYLMRHLC 70
 Qy 12 SSERKEKERSDAARSRSRKESEVYELAHOLPLPHNVSSHLKDASWMLTISYLRVRL 73
 Qy 71 AAGGKGKGATGKLLPPEGGGFRGTHRGKGLPVGKQQA-----PGQSDILC 120
 Db 74 DAG-----DIDIEDDMQKQNCFYKUQALGFWMLTD 105
 Qy 121 SSSLIH----NPTPG-TNFSLIGHISIFDTHPCDQOBELQDALTPRNPNSKKLAP 174
 Db 106 DGMIVYSDAVNKGMLQF-BLTGHSVFDTHPCDHEBEMELTIRNGLYKKGQNT 163
 Qy 175 ERHSLRMKSTLSRGRTNLKATWKVLUHCSGMRAVKPPQQTSPAGSPRSERPLCLV 234
 Db 164 ORSFPLRMKCTLSRGRTNMNIKSATWKVLUHCTGHIHVYDTSNQPGG-YKKPWPMLC 221
 Qy 235 LICEAIP 241
 Db 222 LICEPIP 228

RESULT 9
 US-08-915-213-2
 ; Sequence 2, Application US/08915213
 ; Patent No. 6020462
 ; GENERAL INFORMATION:
 ; APPLICANT: Semenza, Gregg L.
 ; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
 ; NUMBER OF SEQUENCES: 64

RESULT 10
 US-09-148-547-2
 ; Sequence 2, Application US/09148547
 ; Patent No. 6124131
 ; GENERAL INFORMATION:
 ; APPLICANT: Semenza, Gregg L.
 ; TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
 ; FILE REFERENCE: 07265/151001
 ; CURRENT FILING DATE: 1998-08-25
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 826

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/915, 213
 ; FILING DATE: 20-AUG-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480, 473
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07265/053001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 826 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; US-08-915-213-2

Query Match 30.3%; Score 495; DB 3; Length 826;
 Best Local Similarity 46.2%; Pred. No. 3-e-45; Mismatches 59; Indels 48; Gaps 6;
 Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

Qy 11 NTELKEKERSDAARSRSRQETEVYQALHTLPFARGVSAHLKASIMULTISYLMRHLC 70
 Qy 14 SSERKEKERSDAARSRSRKESEVYELAHOLPLPHNVSSHLKDASWMLTISYLRVRL 73
 Qy 71 AAGGKGKGATGKLLPPEGGGFRGTHRGKGLPVGKQQA-----PGQSDILC 120
 Db 74 DAG-----DIDIEDDMQKQNCFYKUQALGFWMLTD 105
 Qy 121 SSSLIH----NPTPG-TNFSLIGHISIFDTHPCDQOBELQDALTPRNPNSKKLAP 174
 Db 106 DGMIVYSDAVNKGMLQF-BLTGHSVFDTHPCDHEBEMELTIRNGLYKKGQNT 163
 Qy 175 ERHSLRMKSTLSRGRTNLKATWKVLUHCSGMRAVKPPQQTSPAGSPRSERPLCLV 234
 Db 164 ORSFPLRMKCTLSRGRTNMNIKSATWKVLUHCTGHIHVYDTSNQPGG-YKKPWPMLC 221
 Qy 235 LICEAIP 241
 Db 222 LICEPIP 228

US-09-438-833-1

Sequence 1, Application US/09438833

PATENT NO. 6436554

GENERAL INFORMATION:

APPLICANT: Pharmacia & Upjohn

TITLE OF INVENTION: Protein variant B

FILE REFERENCE: 1848

CURRENT APPLICATION NUMBER: US/09/438, 833

CURRENT FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 826

TYPE: PRT

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

VOLUME: 92

PAGES: 5510-5514

DATABASE: GenBank U22431

DATABASE ENTRY DATE: 1995-06-28

US-09-438-833-1

Query Match 30.3%; Score 495; DB 4; Length 826; Best Local Similarity 46.2%; Pred. No. 3e-45; Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

QY 11 NTSLRKERSDAARSRSRQSQTETVYQALHTLPARGVS AHLKASIMRLTISYLRMRLC 70

QY 14 SSERKEKRSDAARSRSRKSKESEVFYELAHQLPLPHNVSHLDKASWMLTISYLRKLL 73

QY 71 AAGGKGKGATGRGLPCEGGFRHGRHLQGKPGVKKQQA-----PGPOSVDLC 120

Db 74 DAG-----DLDIEDDKMAQMCNCFYIKALDGFVWVLTID 105

QY 121 SSSLIH----NPTPG-TNFSLELIGHSFDFIHPQDQBLQDALTPRNPNSKKLRAPT 174

Db 106 DGMIVYISDNVNKVMGLQF- ELTGHSVFDTHPCDHEEMLTHRNLTKKGKEQNT 163

QY 175 ERHPSLRMKSTSRSRGTNLKATWKVLUHCGHMRAYKPPQQTSPAGSPRSPRSPQCLV 234

Db 164 QRSFFPLRMKCTLSRGRTMNIKSATWKVLUHCTGHIVHVDTSNSQPOCG- YKKPPMTCLV 221

QY 235 LICEAIP 241

Db 222 LICEPIP 228

QY 106 DGMIVYISDNVNKVMGLQF- ELTGHSVFDTHPCDHEEMLTHRNLTKKGKEQNT 163

Db 105 DLDIEDDKMAQMCNCFYIKALDGFVWVLTID 105

QY 174 DAG-----DLDIEDDKMAQMCNCFYIKALDGFVWVLTID 105

Db 163 DGMIVYISDNVNKVMGLQF- ELTGHSVFDTHPCDHEEMLTHRNLTKKGKEQNT 163

QY 221 QRSFFPLRMKCTLSRGRTMNIKSATWKVLUHCTGHIVHVDTSNSQPOCG- YKKPPMTCLV 221

Db 228 LICEPIP 228

QY 234 ERHPSLRMKSTSRSRGTNLKATWKVLUHCGHMRAYKPPQQTSPAGSPRSPRSPQCLV 234

Db 227 LICEPIP 227

QY 233 LICEAIP 241

Db 226 LICEPIP 226

QY 232 LICEPIP 225

Db 225 LICEPIP 225

QY 231 LICEPIP 224

Db 224 LICEPIP 224

QY 230 LICEPIP 223

Db 223 LICEPIP 223

QY 229 LICEPIP 222

Db 222 LICEPIP 222

QY 228 LICEPIP 221

Db 227 LICEPIP 227

QY 227 LICEPIP 226

Db 226 LICEPIP 226

QY 226 LICEPIP 225

Db 225 LICEPIP 225

QY 224 LICEPIP 224

Db 223 LICEPIP 223

QY 222 LICEPIP 222

Db 221 LICEPIP 221

QY 220 LICEPIP 220

Db 219 LICEPIP 219

US-09-702-705-330

Query Match 30.3%; Score 495; DB 4; Length 826; Best Local Similarity 46.2%; Pred. No. 3e-45; Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6;

QY 11 NTSLRKERSDAARSRSRQSQTETVYQALHTLPARGVS AHLKASIMRLTISYLRMRLC 70

QY 14 SSERKEKRSDAARSRSRKSKESEVFYELAHQLPLPHNVSHLDKASWMLTISYLRKLL 73

QY 71 AAGGKGKGATGRGLPCEGGFRHGRHLQGKPGVKKQQA-----PGPOSVDLC 120

Db 74 DAG-----DLDIEDDKMAQMCNCFYIKALDGFVWVLTID 105

QY 121 SSSLIH----NPTPG-TNFSLELIGHSFDFIHPQDQBLQDALTPRNPNSKKLRAPT 174

Db 106 DGMIVYISDNVNKVMGLQF- ELTGHSVFDTHPCDHEEMLTHRNLTKKGKEQNT 163

QY 175 ERHPSLRMKSTSRSRGTNLKATWKVLUHCGHMRAYKPPQQTSPAGSPRSPRSPQCLV 234

Db 164 QRSFFPLRMKCTLSRGRTMNIKSATWKVLUHCTGHIVHVDTSNSQPOCG- YKKPPMTCLV 221

QY 235 LICEAIP 241

Db 222 LICEPIP 228

QY 106 DGMIVYISDNVNKVMGLQF- ELTGHSVFDTHPCDHEEMLTHRNLTKKGKEQNT 163

Db 105 DLDIEDDKMAQMCNCFYIKALDGFVWVLTID 105

QY 221 QRSFFPLRMKCTLSRGRTMNIKSATWKVLUHCTGHIVHVDTSNSQPOCG- YKKPPMTCLV 221

Db 220 LICEPIP 220

QY 229 LICEPIP 225

Db 228 LICEPIP 228

QY 228 LICEPIP 224

Db 227 LICEPIP 227

QY 227 LICEPIP 223

Db 226 LICEPIP 226

QY 226 LICEPIP 225

Db 225 LICEPIP 225

QY 224 LICEPIP 224

Db 223 LICEPIP 223

QY 223 LICEPIP 222

Db 222 LICEPIP 222

QY 222 LICEPIP 221

Db 221 LICEPIP 221

QY 220 LICEPIP 220

Db 219 LICEPIP 219

QY 221 LICEPIP 221

Db 220 LICEPIP 220

QY 222 LICEPIP 222

Db 221 LICEPIP 221

QY 223 LICEPIP 223

Db 224 LICEPIP 224

QY 225 LICEPIP 225

Db 226 LICEPIP 226

QY 227 LICEPIP 227

Db 228 LICEPIP 228

QY 229 LICEPIP 229

Db 220 LICEPIP 220

QY 221 LICEPIP 221

Db 222 LICEPIP 222

QY 223 LICEPIP 223

Db 224 LICEPIP 224

QY 225 LICEPIP 225

Db 226 LICEPIP 226

QY 227 LICEPIP 227

Db 228 LICEPIP 228

QY 229 LICEPIP 229

Db 220 LICEPIP 220

QY 221 LICEPIP 221

Db 222 LICEPIP 222

QY 223 LICEPIP 223

Db 224 LICEPIP 224

QY 225 LICEPIP 225

Thu Jun 16 13:05:39 2005

us-09-896-791b-3.rai

Page 7

Db 164 QRSFPLRMKCTLTSGRTMNIKSATWKVLHCTGHIHVYDINNSNQPQCG--YKKPMTCLV 221

QY 235 LICEALP 241
| | | | |
222 LICEPIP 228

Search completed: June 15, 2005, 16:01:42
Job time : 43 sec_B

ایجادی یعنی
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CC inhibiting angiogenesis, particularly where associated with ischaemic cardiovascular lesions, stroke or diabetic microvascular diseases; and CC tumour growth. This is the amino acid sequence of the mouse inhibitor CC PAS domain protein (IPAS), described in the method of the invention
XX SQ

(ANGI-) ANGIOGENETICS SWEDEN AB
Makino Y, Cao Y, Poellinger L;
WPI; 2003-505168/47.
N-PSDB; ACC03867.

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Query Match          100.0%; Score 1636; DB 5; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.9e-160;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

New pharmaceutical composition comprising IPAS, useful for increasing angiogenesis, or for treating a hypoxia-mediated condition in a cell, group of cells or organisms under hypoxic conditions, e.g. stroke or

Sequence 307 AA

RESULT 2
ABR62227
ID ABR62227 standard; protein; 307 AA.
XX

Query	Match	100 %;	Score 1636;	DB 6;	Length 307;
Best Local Similarity		100.0 %;	Pred. No. 1.	9e-160;	
Matches	307;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;

QY	61	ISYLRMFLCAAGGKRGRATORGLLPBGGGRHGRHGRHLGVCKCQ21PGPQSVDLC	120
Db	61	ISYLRMFLCAAGGKRGRATORGLLPBGGGRHGRHGRHLGVCKCQ21PGPQSVDLC	120
	61	ISYLRMFLCAAGGKRGRATORGLLPBGGGRHGRHGRHLGVCKCQ21PGPQSVDLC	120

QY	181	RWKSTLTSRGTTNLQKATWKVQHSGHMRAYKPPQTSRSPGSRSPEPPQQCLVILCEAI	240
Db	181	RWKSTLTSRGTTNLQKATWKVQHSGHMRAYKPPQTSRSPGSRSPEPPQQCLVILCEAI	240
Qy	241	POLPFIDGATGLPQSKTPSTLFTPLWKAICLCLVLRWPVQVQLOGKGTESLSPWMLWAL	300
Db	241	POLPFIDGATGLPQSKTPSTLFTPLWKAICLCLVLRWPVQVQLOGKGTESLSPWMLWAL	300
QY	301	NRKNCPG 307	
Qy	301	NRKNCPG 307	

RESULT 3
 ABR83343 standard; protein; 324 AA.
 ABR83343;
 AC
 AC
 DT 06-OCT-2003 (first entry)
 XX
 XX

DE	Human NOV9a protein SEQ ID NO:20.	Qy	181 RMKSTLTSRGRTINAKAATWVKGSGHRAKPAQTSAGSPSEPPFQCLVILCEAI 240
KW	Human; NOV9; cytostatic; antidiabetic; neuroprotective; anti-parkinsonian; anorectic; gene therapy; vaccine; cancer; neurodegenerative disorder; Parkinson's disease; metabolic disorder; diabetes; obesity; tissue typing.	Db	181 RMKSTLTSRGRTINAKAATWVKGSGHRAKPAQTSAGSPSEPPFQCLVILCEAI 240
KW	Homo sapiens.	Qy	241 FPLPFHDGATIGLPLQEKAA-TSPPLSPVYVGRHCSICFVREWP-IQIGANGMSDPSLIP 294
OS		Db	241 FPLPFHDGATIGLPLQEKAA-TSPPLSPVYVGRHCSICFVREWP-IQIGANGMSDPSLIP 294
PN	WO2003052061-A2.	Qy	295 WVLWALNRKNCPG 307
PD	26-JUN-2003.	Db	299 EVMWAINGGNAG 311
XX			
XX	03-DEC-2002; 2002WO-US038821.		
XX			
PR	17-DEC-2001; 2001US-0341477P.		
PR	17-DEC-2001; 2001US-0341540P.		
PR	20-DEC-2001; 2001US-03422592P.		
PR	31-DEC-2001; 2001US-0344903P.		
PR	17-APR-2002; 2002US-0373288P.		
PR	15-MAY-2002; 2002US-0380981P.		
PR	17-MAY-2002; 2002US-0381495P.		
PR	28-MAY-2002; 2002US-0383744P.		
PR	29-MAY-2002; 2002US-0384024P.		
PR	07-AUG-2002; 2002US-0301788P.		
PR	26-AUG-2002; 2002US-0406353P.		
PR	31-OCT-2002; 2002US-0422756P.		
PR	02-DEC-2002; 2002US-00307928.		
PA	(CURA-) CURAGEN CORP.		
XX			
XX	Alsobrook JP, Anderson DW, Boldog FL, Burgess CB, Catterton B; PT Edinger SR, Gorman L, Guo X, Ji W, Kekuda R, Li L, Patturajan M; Rieger DK, Shenoy SG, Spytek KA, Vernet CAM, Voss EZ, Zhong M; WPI; 2003-533005/50.		
PT	New NOV9 polypeptide, useful for preparing a composition for treating or preventing e.g. cancer, neurodegenerative disorders such as Parkinson's disease, or metabolic disorders such as diabetes or obesity, or for tissue typing.		
PT			
XX			
XX	ACF06242 to ACF06242 encode the human NOV9 proteins given in ABR83334 to ABR83343, designated NOV9a, NOV9a, NOV9a, NOV9a, NOV9a, NOV9a, NOV9a, NOV9a and NOV9a respectively. NOV9 sequences can have cytostatic, antidiabetic, neuroprotective, anti-parkinsonian and anorectic activities, and can be used in vaccines and gene therapy. The NOV9 polypeptides can be used for preparing a composition for treating or preventing a pathology associated with the NOV9-polypeptides e.g. cancer, neurodegenerative disorders such as diabetes or obesity, or metabolic disorders such as diabetes or obesity, or for tissue typing		
XX			
XX	Claim 1; Page 130; 190pp; English.		
PS			
PS	ACF06243 to ACF06242 encode the human NOV9 proteins given in ABR83334 to ABR83343, designated NOV9a, NOV9a, NOV9a, NOV9a, NOV9a, NOV9a, NOV9a, NOV9a and NOV9a respectively. NOV9 sequences can have cytostatic, antidiabetic, neuroprotective, anti-parkinsonian and anorectic activities, and can be used in vaccines and gene therapy. The NOV9 polypeptides can be used for preparing a composition for treating or preventing a pathology associated with the NOV9-polypeptides e.g. cancer, neurodegenerative disorders such as diabetes or obesity, or metabolic disorders such as diabetes or obesity, or for tissue typing		
PS	Sequence 324 AA;		
PS	Query Match 78.1%; Score 1278; DB 6; Length 324; Best Local Similarity 79.9%; Pred. No. 2.5e-123; Matches 250; Conservative 14; Mismatches 41; Indels 8; Gaps 3;		
PS	Sequence 324 AA;		
PS	Query Match 78.1%; Score 1278; DB 6; Length 324; Best Local Similarity 79.9%; Pred. No. 2.5e-123; Matches 250; Conservative 14; Mismatches 41; Indels 8; Gaps 3;		
CC	The present sequence represents mouse MOP7, a novel member of the PAS superfamily, where PAS stands for PER/ANRT/SIM domains. MOP7 cDNA (see AX5896) was identified in a search of murine ESTs designed to identify bHLH-PAS proteins, and by RACE amplification of lung cDNA. MOP7 was characterised as hypoxia inducible factor 3 alpha (HIF 3 alpha). Its expression profile is distinct from that of HIF 1 alpha (see AAY06291), HIF 2 alpha (see AAY06290), MOP3 (see AAY05291), Ah receptor and Ah receptor nuclear translocator (ARNT), suggesting a different functional role. MOP7 probably regulates the same genes as HIF 1 alpha and 2 alpha, as evidenced by its dimerisation with the same partners (ARNT, MOP3) and recognition of the same core response element. MOP7 may have a functional role associated with response to low oxygen in the tissues in which it is expressed. The invention provides novel MOPs 2-9 nucleic acids (see AX58981-88) and proteins (see AAY06299-97). These are useful in a variety of research, diagnostic and therapeutic applications. Several of the MOPs are alpha-class hypoxia-inducible factors. Others are involved in circadian signal transduction		
CC			
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
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CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Indels 55; Gaps 4;		
CC	Sequence 62 AA;		
CC	Query Match 52.3%; Score 855.5; DB 2; Best Local Similarity 68.4%; Pred. No. 4.2e-79; Matches 182; Conservative 5; Mismatches 24; Ind		

Db 7 RSNTEFLRKSKRDAARSRSQETEVLYQLAHTLPPARGVSAHDKASIMRLTISYLMER 66
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAB93166 to AAH13628 and
 CC AAH13633 to AAH13642 represent human cDNA sequences; AAB92446 to AAH13629 represent
 CC human amino acid sequences; and AAB9332 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention.

Db 121 - SSSLTHNPTGTFNS-LELIGHISIDFPDIHPCDQEELQDALTPRNTLSKCL 170
 CC

Db 95 MVVLTAAEGDMAYISENVSKHGLISQLEBLIGHISIDFPDIHPCDQEELQDALTPRNTLSKCL 154
 CC

Db 171 EAPTERHFSLARKMKSTLTSGRNTLNKAATKVKLHCSGHMRAYKPAQTSPPSPRSEPL 230
 CC

Db 155 EAPTERHFSLARKMKSTLTSGRNTLNKAATKVKLHCSGHMRAYKPAQTSPPSPRSEPL 214
 CC

Qy 231 QCLVIVICEAIP---QLPFHDGATL 251
 CC

Db 215 QCLVIVICEAIPHPASLEPPLGAFL 240
 CC

RESULT 5

AAB93326
 ID AAB93326 standard; protein; 632 AA.
 XX

AC AAB93326;
 XX

DT 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:12422.
 XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 OS Homo sapiens.
 XX

PR 09-JUN-2000; 20000P-00183767.
 PR 09-JUN-2000; 20000P-00241899.
 PN EP1074617-A2.
 XX

PD 07-FEB-2001.
 XX

PF 28-JUL-2000; 20000P-00116126.
 XX

PR 29-JUL-1999; 990P-00248036.
 PR 27-AUG-1999; 990P-00300253.
 PR 11-JAN-2000; 20000P-00118775.
 PR 02-MAY-2000; 20000P-00183767.
 PR 09-JUN-2000; 20000P-00241899.
 PA (HELI-) HELIX RES INST.
 XX

PT Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.;
 PI Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T.;
 XX WPI; 2001-310749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 PT

XX

PS Claim 8; SEQ ID NO 12422; 2537PP + Sequence Listing; English.
 XX

CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the combination
 CC of oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in the
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC

Query Match 50.8%; Score 831; DB 4; Length 632;
 Best Local Similarity 68.2%; Pred. No. 1.4e-76; Mismatches 30; Indels 42; Gaps 5;
 Matches 178; Conservative 11; Sequence 632 AA;

Qy 1 MAIGLORVRSNTLKRKSKRDAARSRSQETEVLYQLAHTLPPARGVSAHDKASIMRLT 60
 DB 1 MAIGLORRSTBLKRKSKRDAARSRSQETEVLYQLAHTLPPARGVSAHDKASIMRLT 60
 Qy 61 ISVLMRHLCAAGGKRGRATGRLLPGCRRGGFRHGRHGRHLGVKQ----- 109
 DB 61 ISVLMRHLCAAG----- 100
 Qy 110 QAPGQPOSUDLCSSSLHNPPTGTFNS-LELIGHISIDFPDIHPCDQEELQDALTPRPLSKK 168
 DB 101 TAEGDMA----LSENTHGIGLSELELIGHISIDFPDIHPCDQEELQDALTPQQLRSR 154
 Qy 169 KLEAPTERHFSLARKMKSTLTSGRNTLNKAATKVKLHCSGHMRAYKPAQTSPPSPRSEPL 228
 DB 155 KLEAPTERHFSLARKMKSTLTSGRNTLNKAATKVKLHCSGHMRAYKPAQTSPPSPRSEPL 214
 Qy 229 PQLVIVICEAIPQLPFHDGA 249
 DB 215 PQLVIVICEAIP---HPGS 231

RESULT 6

AA016439
 ID AA016439 standard; protein; 790 AA.
 XX

AC AA016439;
 XX

DT 10-APR-2003 (first entry)

XX Human nucleic acid-associated protein (NAAP) - SEQ ID NO 36.
 XX

KW Human; nucleic acid-associated protein; NAAP; arteriosclerosis; AIDS;
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; asthma;
 KW developmental disorder; renal tubular acidosis; anaemia; epilepsy;
 KW mental retardation; neurologic disorder; Alzheimer's disease; epilepsy;
 KW Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy;
 KW Crohn's disease; transgenic animal; animal model.

OS Homo sapiens.
 XX

PN W02003000864-A2.
 XX

PD 03-JAN-2003.

XX

PF 20-JUN-2002; 2002W0-US021179.

XX

PR 22-JUN-2001; 2001US-0300518P.
 PR 29-JUN-2001; 2001US-0301787P.
 PR 29-JUN-2001; 2001US-0301792P.
 PR 29-JUN-2001; 2001US-0301822P.
 PR 29-JUN-2001; 2001US-0301833P.
 PR 06-JUL-2001; 2001US-0303405P.
 PR 06-JUL-2001; 2001US-0303422P.
 PR 15-MAR-2002; 2002US-0364438P.
 XX

PA (INCY-) INCYTE GENOMICS INC.

XX Gandhi, AR, Swarnakar, A, Hafalia, AJ, Warren, BA, Emerging BM;

PI Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe IJ;
 PI Ramkumar J, Griffin JA, Yang J, Sanjanawala MM, Baugh MK;
 PI Borowsky ML, Yao MG, Walia NM, Bandhan O, Lal PG, Becha SD, Lee SY;
 PI Richardson TM, Elliott VS, Luo W, Tang YR, Zebarjad Y, Lu Y;
 XX DR WPI; 2003-201420/19.
 DR N-PSDB; AAL51589.
 XX PT New nucleic acid-associated proteins and polynucleotides, useful for
 PT diagnosing, treating or preventing cell proliferative (e.g. cancer),
 PT neurological (e.g. epilepsy or Parkinson's disease), or autoimmune
 PT disorders (e.g. AIDS).
 XX PS Claim 1; Page 274-276; 312pp; English.
 CC The invention comprises the amino acid and coding sequences of human
 CC nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
 CC the invention are useful for diagnosing, treating or preventing disorders
 CC associated with aberrant expression of NAAP, such as: cell proliferative
 CC disorders (e.g. arterioclerosis, atherosclerosis, cirrhosis, hepatitis,
 CC or mental retardation); neurological disorders (e.g. Alzheimer's disease,
 CC Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders
 CC (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of
 CC the invention are useful for creating transgenic animals to model human
 CC associated protein of the invention.
 XX SQ Sequence 790 AA;

Query Match 49.1%; Score 803; DB 6; Length 790;
 Best Local Similarity 58.7%; Pred. No. 1.5e-73; Gaps 6;
 Matches 179; Conservative 11; Mismatches 29; Indels 86; Gaps 6;
 Qy 1 MALGIQVR-----SNTELRK 16
 Db 1 MALGIQVRPAISCCVISPPCAPTRNSHRCGCTASPPAPPQGWPFSQRCPGRMSTELRK 60
 Qy 17 EKSRAARSRSQETEVLYQLAHTLPFARGVSVAHDKASIMRLTISYLRMRHLCAAGGER 76
 Db 61 EKSRAARSRSQETEVLYQLAHTLPFARGVSVAHDKASIMRLTISYLRMRHLCAAG--- 117
 Qy 77 GRATGRLLPBGPGGSPRHGTHRGHGLPVGKQ-----QAPGQSVQDCLSSLI 125
 Db 118 -----EMNQVGAGGERPLDACYLAKLEGFFVMVLTAEQDMAY-----LS 154
 Qy 126 HNPTPGTINFS-LELGHSTPDFIHCQDQEQLDQALTPRNLSKKLEAPERHSLRMS 184
 Db 155 ENVSKHGLSQELELGHSTPDFIHCQDQEQLDQALTPQQTLSRKVEATERCSLRMS 214
 Qy 185 TLTSGRTLNLKAATWKVLSGMRAYKPAQTSPPASPRSPSERPLQCLVLTCAIPOLP 244
 Db 215 TLTSGRTLNLKAATWKVLSGMRAYKPAQTSPPASPRSPSERPLQCLVLTCAIP--- 271
 Qy 245 FHDGA 249
 Db 272 -HPGS 275

, RESULT 7
 AAB24222
 ID AAB24222 standard; protein; 667 AA.
 XX AC AAB24222;
 XX DT 23-SEP-2002 (first entry)
 XX DB Human HIF-3 protein.

KW angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;
 KW polycythaemia vera; hypoxia responsive element; HRE.
 XX OS Homo sapiens.
 XX PN WO20032291-A2.
 XX PD 02-MAY-2002.
 XX PR 25-OCT-2001; 2001WO-US049856.
 XX PR 26-OCT-2000; 2000US-0243542P.
 XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX PI Colgan SP;
 DR N-PSDB; AAD39042.
 XX WPI; 2002-471427/50.
 XX Treating a subject (at risk of) having a hematologic malignancy or
 PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia
 PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
 PT binding molecules.
 XX Disclosure; Page 88-91; 92pp; English.
 CC The invention relates to a method of treating a subject having or at risk
 CC of developing a hematologic malignancy or multidrug resistance (MDR).
 CC The method involves administering hypoxia inducible factor-1 (HIF-1)
 CC binding molecules or small ubiquitin-like-modifier (SMO)1 binding
 CC molecules or HIF-1-SMO-1 complex modulators. Anti-hypoxia responsive
 CC element (HRE) binding molecules or antisense nucleic acid molecules and
 CC SMO-1 binding molecules or antisense molecules are useful for treating a
 CC subject having or at risk of developing hematologic malignancy or MDR
 CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
 CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
 CC e.g. Lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
 CC disorders include chronic or acute myeloid leukaemia, e.g. angiogenic
 CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
 CC invention is used in gene therapy. The present sequence is human HIF-3
 CC protein.
 XX SQ Sequence 667 AA;

Query Match 49.0%; Score 802; DB 5; Length 667;
 Best Local Similarity 68.0%; Pred. No. 1.5e-71; Gaps 5;
 Matches 172; Conservative 11; Mismatches 28; Indels 42; Gaps 5;
 Qy 9 RSNTELRKSKRDAARSRSQETEVLYQLAHTLPFARGVSVAHDKASIMRLTISYLRMR 68
 Db 7 RSTTELRKSKRDAARSRSQETEVLYQLAHTLPFARGVSVAHDKASIMRLTISYLRMR 66
 Qy 69 LCAAGKGKGRATGRLLPBGPGGSPRHGTHRGHGLPVGKQ-----QAPGQSV 117
 Db 67 LCAGG-----EMNQVGAGGERPLDACYLAKLEGFFVMVLTAEQDMAY 106
 Qy 118 DCGSSLTHNPTPGTINFS-LELGHSTPDFIHCQDQEQLDQALTPRNLSKKLEAPER 176
 Db 107 -----EMNQVGAGGERPLDACYLAKLEGFFVMVLTAEQDMAY 160
 Qy 177 HFSLRMKSTLTSRGRTLNLKAATWKVLSGMRAYKPAQTSPPASPRSPSERPLQCLVLI 236
 Db 161 CFSLRMKSTLTSRGRTLNLKAATWKVLSGMRAYKPAQTSPPASPRSPSERPLQCLVLI 220
 Qy 237 CEALPQLDFHDGA 249
 Db 221 CEAIP---HPGS 229

KW Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;
 KW hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-3;
 KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
 KW myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;

XX
AC AAO16417;
XX
DT 10-APR-2003 (first entry)
XX
DE Human nucleic acid-associated protein (NAAP) - SEQ ID No 14.
XX
KW Human; nucleic acid-associated protein; NAAP; arteriosclerosis; cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS; cancer; developmental disorder; renal tubular acidosis; anaemia; asthma; mental retardation; neurological disorder; Alzheimer's disease; epilepsy; Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy; Crohn's disease; transgenic animal; animal model.
XX
OS Homo sapiens.
XX
PN WO20030008864-A2.
XX
PD 03-JAN-2003.
XX
PP 20-JUN-2002; 2002WO-US021179.
XX
PR 22-JUN-2001; 2001US-0300518P.
PR 29-JUN-2001; 2001US-0301787P.
PR 29-JUN-2001; 2001US-0301792P.
PR 29-JUN-2001; 2001US-0301892P.
PR 29-JUN-2001; 2001US-0301893P.
PR 06-JUL-2001; 2001US-0303405P.
PR 15-MAR-2002; 2002US-0364438P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PT Gandhi AR, Swarnkar A, Hafalia AJA, Warren BA, Emerling BM; PI Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forysthe IJ; PI Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Bandman O, Ial PG, Becha SD, Lee SY; PI Borowsky MI, Yao MG, Walla NK, Bandman O, Ial PG, Becha SD, Lee SY; PT Richardson TW, Elliott VS, Luo W, Tang YT, Zebarjad Y, Lu Y; DR WPI; 2003-201420/19.
DR N-FSDB; ABK1567.
XX
PT New nucleic acid-associated proteins and polymucleotides, useful for diagnosing, treating or preventing cell proliferative (e.g. cancer), neurological (e.g. epilepsy or Parkinson's disease), or autoimmune disorders (e.g. AIDS).
XX
PS Claim 1; Page 232-234; 312pp; English.
XX
PT The invention comprises the amino acid and coding sequences of human nucleic acid-associated proteins (NAAP). The DNA and protein sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of NAAP, such as: cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation); neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of the invention are useful for creating transgenic animals to model human disease. The present amino acid sequence represents a human nucleic acid- associated protein of the invention
XX
SQ Sequence 747 AA;
Query Match 48.7%; Score 797.5; DB 6; Length 747;
Best Local Similarity 60.4%; Pred. No. 5.2e-73;
Matches 180; Conservative 10; Mismatches 35; Indels 73; Gaps 6;
Oy 1 MALGQVRV-----SNTELRK 16
Db 1 MALGQRARPLASCCVISPCCAPTRNSHPGCTASPPARPGWPFSSORGPRWNSTELRK 60
Oy 17 EKSDRARRRSQEVIVVQIAVTPAKGSANIKASIMRITISVHMRICAGGR 76

Do 61 EKSDRARRRSQEVIVVQIAVTPAKGSANIKASIMRITISVHMRICAGGR 120
Oy 77 GRATGR---LPIEGPGCFRGRGHRGRGHLPGVGKCOQAPGPOSVUCCSSLHNTPG 132
Db 121 QVAGENHWWMLKALECFVWMLTAEG-----DM--AXLSENISKHL 160
Oy 133 NFS-LELIGHSIFDPTRPCDQEELQDALTTPRNLSKCKLEAPTERHFSLRMKSTLSRG 191
Db 161 GLSQLELIGHSIFDFIFHPCDQEELQDALTTPQQLTSRKVEAPTERCFSLRMKSTLSRG 220
Oy 192 TNLKAATWKVLUHCSGHMRAYKPPQTSPPASPRSPRSPQLCVLUCEAIP---HPG 249
Do 221 TNLKAATWKVLUHCSGHMRAYKPPQTSPPASPRSPQLCVLUCEAIP---HPG 274

RESULT 9
ABG66737
ID ABG66737 standard, protein, 407 AA.
XX
AC ABG66737;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human novel polypeptide #72.
XX
Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematoopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; repartusus injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolytic; thrombosis; coagulation disorder; fungal infection.
XX
OS Homo sapiens.
XX
PN WO20024340-A2.
XX
PD 06-JUN-2002.
XX
PT 30-NOV-2001; 2001WO-US047004.
XX
PR 30-NOV-2000; 2000US-00728952.
XX
PA (HYSE-) HYSEQ INC.
XX
PT Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D; PI Yamazaki V, Ujjwal ML, Dumanac RT; DR WPI; 2002-508509/54.
DR N-FSDB; ABK94961.
XX
PT Novel nucleic acids and polypeptides for diagnosis, treatment of, inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing.
XX
PS Claim 10; Page 649; 672pp; English.
XX
PT The invention relates to human novel polymucleotides and associated polypeptides. The polymucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haemopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue

CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
 CC disease. The sequences of the invention are also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC including severe combined immunodeficiency (SCID), bacterial or fungal
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
 CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic
 CC and coagulation disorders. Sequences ABG66666-ABC66758 represent human
 CC novel polypeptides of the invention
 XX Sequence 407 AA;

Query Match 48.7%; Score 797; DB 5; Length 407;
 Best Local Similarity 67.9%; Pred. No. 2.4e-73; Mismatches 171; Conservatve 11; Indels 42; Gaps 5;
 Matches 28;

QY 10 SNTTELKEKSRDAARSRSRQQETEVLYQLAHTLPFARGVS AHLDKASIMRLTISYLRMHL 69
 54 SNTTELKEKSRDAARSRSRQQETEVLYQLAHTLPFARGVS AHLDKASIMRLTISYLRMHL 113

Db 70 CAAGSKRGRATGRILLPGEGPGFRHGRHGRGLPGVKQO-----QAGPQSTD 118
 114 CAAG-----EWNQVAGGEPDACYLKALEGFWMLTAEQDMAY- 152

QY 119 LCSSSLIHNTPGTINPS-LELIGHSTIDFIRHCDQELQDALTPOQTLURRKVERAPTERH 177
 153 ---LSENVSKHIGLQSLIGHISIDFIRHCDQELQDALTPOQTLURRKVERAPTERC 207

QY 178 FSLRMKSTLTSRGRTLNKAAATWKVLUHCSCHMRAYKPAOTS PAGSPRSEPPQCLVLC 237

Db 208 FSLRMKSTLTSRGRTLNKAAATWKVLUHCSCHMRAYKPAOTS PAGSPDSEPPQCLVLC 267

QY 238 RAIPOLPFDGA 249
 268 RAIP---HPGS 275

Db

RESULT 10

AAB34826
 ID AAB34826 standard; protein; 705 AA.
 XX
 AC AAB34826;
 XX
 DT 28-MAY-2003 (first entry)

DB Human hypoxia inducible factor (HIF)-1alpha protein.

XX Human; hypoxia inducible factor; HIF-1alpha; tumour; muscular function;
 KW vascular endothelial growth factor; vEGF; angiogenesis; cardiovascular;
 KW coronary disease; cardiac disease; cytostatic; Cardiant; cell survival;
 OS Homo sapiens.
 XX
 PN WO200294862-A2.

XX
 PD 28-NOV-2002.

XX
 PR 23-MAY-2002; 2002WO-CA000752.

XX
 PR 23-MAY-2001; 2001US-022630P.
 PR 08-FEB-2002; 2002US-035452P.

PA (ANGI-) ANGIOGENE INC.

XX
 PT Guy L;
 XX
 DR WPI; 2003-129410/12.
 DR N-FSDB; AAD53131.

XX
 PT New Hypoxia Inducible Factor-3 alpha polynucleotide for inducing vascular
 PT endothelial growth factor (VEGF) expressions in a tissue or cell,
 particularly for eliminating tumors, or treating coronary or cardiac

PT diseases in mammals.
 XX
 PS Claim 13; Col 69-72; 38pp; English.

XX
 The invention relates to hypoxia inducible factor (HIF)-1alpha DNA and
 CC protein sequences. The HIF-1alpha DNA and protein sequences are useful
 CC for inducing vascular endothelial growth factor (VEGF) expression or
 CC angiogenesis in a mammalian tissue or cell, for modulating tumoural cell
 CC survival, eliminating a tumoural cell, or evaluating the malignancy of a
 CC tumour in a subject. They are also useful for improving muscular
 CC function, particularly for treating coronary and cardiac diseases in
 CC mammals. The present sequence is human HIF-1alpha protein.
 XX
 Sequence 705 AA;

Query Match 48.6%; Score 795; DB 6; Length 705;
 Best Local Similarity 67.6%; Pred. No. 8.6e-73; Mismatches 171; Conservatve 11; Indels 42; Gaps 5;
 Matches 29;

QY 9 RSNTTELKEKSRDAARSRSRQQETEVLYQLAHTLPFARGVS AHLDKASIMRLTISYLRMHL 68
 3 RSTTELKEKSRDAARSRSRQQETEVLYQLAHTLPFARGVS AHLDKASIMRLTISYLRMHL 62

Db 69 LCAGGKGRGRATGRILLPGEGPGFRHGRHGRGLPGVKQO-----QAGPQSV 117
 63 LCAG-----EWNQVAGGEPDACYLKALEGFWMLTAEQDMAY- 102

QY 118 DCGSSSLIHNTPGTINPS-LELIGHSTIDFIRHCDQELQDALTPOQTLURRKVERAPTERH 176
 103 ---LSENVSKHIGLQSLIGHISIDFIRHCDQELQDALTPOQTLURRKVERAPTER 156

QY 177 FSLRMKSTLTSRGRTLNKAAATWKVLUHCSCHMRAYKPAOTS PAGSPRSEPPQCLVLC 236
 157 CFSLRMKSTLTSRGRTLNKAAATWKVLUHCSCHMRAYKPAOTS PAGSPDSEPPQCLVLC 216

QY 237 CEATPOLPFDGA 249
 217 CEATIP---HPGS 225

Db

RESULT 11

AAB94934
 ID AAB94934 standard; protein; 648 AA.
 XX
 AC AAB94934;
 XX
 DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:16415.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.

XX
 PR 28-JUL-2000; 2000BP-00116126.

XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-001183767.
 PR 09-JUN-2000; 2000JP-00241899.

XX
 PA (HELI-) HELIX RES INST.
 XX
 Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PT Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the protein encoded by the full-length cDNAs.

PT

XX

PS Claim 8; SEQ ID NO 16415; 2537PP + Sequence Listing; English.

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dt primer and an oligonucleotide which is complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the 5602 oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH1366 to AAH1368 and AAH1363 to AAH18742 represent human cDNA sequences; AAB92446 to AAB9593 represent human amino acid sequences; and AAH1362 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

CC

CC Sequence 648 AA;

Query Match 35.0%; Score 573; DB 4; Length 648; Best Local Similarity 61.0%; Pred. No. 7.7e-50; Matches 125; Conservative 11; Mismatches 27; Indels 42; Gaps 5;

QY 57 MRLTISYLRMLRCAAGGRRGRATGRILPPEGGGFRGHTRGRHGLVNGKQ----- 109

Db 1 MRLTISYLRMLRCAAGGRRGRATGRILPPEGGGFRGHTRGRHGLVNGKQ----- 109

QY 110 ---OAPGPOSVDLCSLILHNPPIGNTNS-LELIGHSTFDIHPCDQBELQDALTRPRN 164

Db 41 WMLTREGMAY----ISBNVSKGLGISOLENLIGHSIFDFIHPCDQBELQDALTRPRN 94

QY 165 LSKKKLEAPTERHFSRMLKSTLTSRGRTNLKAATWKVHLCSGHMRAYKPPA 224

Db 95 LSRKVEAPTERCFSLRMKSTLTSRGRTNLKAATWKVHLCSGHMRAYKPPA 154

QY 225 RSEPLQCLVILICEAIQPLPHDGA 249

Db 155 DSEPLQCLVILICEAIQPLPHDGA 175

RESULT 12

AAH93710 ID AAB93710 standard; protein; 199 AA.

AC AAL93710;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:13303.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000BP-00116126.

XX

PA (HBLI-) HELIX RES INST.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118767.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PR

XX

PR Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PR Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PR Primer sets for synthesising polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX

PS Claim 8; SEQ ID NO 13303; 2537PP + Sequence Listing; English.

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dt primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the 5602 oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs easily without any specialised methods. AAH03166 to AAH1368 and AAH1363 to AAH18742 represent human cDNA sequences; AAB92446 to AAB9593 represent human amino acid sequences; and AAH1362 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

CC

CC Sequence 199 AA;

Query Match 31.7%; Score 518.5; DB 4; Length 199; Best Local Similarity 68.0%; Pred. No. 6.2e-45; Matches 104; Conservative 9; Mismatches 13; Indels 27; Gaps 2;

QY 120 CSSLTIRNPPTGNTNF-----SLELIGHSHIFDFIHPCDQBELQ 156

Db 14 CTSWLTRCPSPAAASAPTWTRPLSCASPSATCACTASAPQLELIGHSHIFDFIHPCDQBELQ 73

QY 157 DALTPRENTLSKKEAPTERHFSRMLKSTLTSRGRTNLKAATWKVHLCSGHMRAYKPPA 216

Db 74 DALTPRENTLSRKKVEAPTERCFSLRMKSTLTSRGRTNLKAATWKVHLCSGHMRAYKPPA 133

QY 217 QTPSPAGSRPSEPLQCLVILICEAIQPLPHDGA 249

Db 134 QTPSPAGSRPSEPLQCLVILICEAIQPLPHDGA 162

RESULT 13

ADL16229 ID ADL16229 standard; protein; 513 AA.

XX

AC ADL16229;

XX

DT 22-APR-2004 (first entry)

XX

DB Human nucleic acid-associated protein (NaAP) #14.

XX

KW human; nucleic acid-associated protein; NaAP; autoimmune disorder;

Sequence	827 AA;	Best Local Similarity	30.4%;	Score	498;	DB	8;	Length	827;
Matches	115;	Conservative	46.2%;	Pred.	No.	6	5e-42;		
Matches	115;	Conservative	26;	Mismatches	60;	Indels	48;	Gaps	6;
QY	9	RSNTTELKEKSRSRDAARSRSRQSEETEVLYQALHTLPPARGVSALHDKQASIMRLTISYRMRH	68						
Db	13	RLSERRKEKSRSRDAARSRSRQSEEVYFLAHOPLPHRNVSSHLDKASAVMRLLTISYLRVK	72						
QY	69	LCANGKGRGRATORGLLPGPQGGFRHGTHTRRGRHGLPLPGKQQA-----PGQSVD	118						
Db	73	LLDAG-----DLDIETDDMKAQMMCFLKALDGFTWNL	104						
QY	119	LCSSSLIH----NPTPG-TNFSLELGHSTDFIHPQCDQEELQDALTPRPNLISKKLEA	172						
Db	105	TDDGDMIVLISDNVNNKYMGLQP--ELTCHSYFDFTHPCDHEEMREMLTHRNLVKGKEQ	162						
QY	173	PTERHFSLRMKSTLTSRGRTLNLKAATWKVHLCSGHNRAKYRPAQTPSPAGSPRSEPLQC	232						
Db	163	NTQRSFFLRLMKCTLTSGRTWMNIKSAATWKVHLCTGHIVYDTSNQPOCG--YKKPWT	220						
QY	233	LVVLECAIP	241						
Db	221	LVVLECAIP	229						